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OM protein - protein search, using BW model

Run on: October 4, 2005, 18:34:55 ; Search time 166 Seconds
(without alignment)
146.783 Million cell updates/sec

Title: US-10-669-175-1
Perfect score: 327
Sequence: 1 ALENLVVNAASAGTHGIL.....LLGLWPLLLLLLPQRAYA 63

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	283	86.5	283	AAR29852	Aar29852 HCV NS2-N
2	283	86.5	480	AAR34002	Aar34002 BK E2/NS1
3	283	86.5	3010	AAR20111	Aar20111 Non-A, no
4	283	86.5	3010	AAR20091	Aar20091 Non-A, no
5	283	86.5	3010	AAV06423	AAV06423 Non-A, no
6	281	85.9	1026	ADJ82984	ADJ82984 Adenovect
7	281	85.9	2307	AAV70064	AAV70064 Recombina
8	281	85.9	2307	AAV70065	AAV70065 Recombina
9	281	85.9	2307	AAV70066	AAV70066 Recombina
10	281	85.9	3010	ABG32458	ABG32458 Hepatitis
11	281	85.9	3010	ABG32459	ABG32459 Hepatitis
12	281	85.9	3010	ABG32451	ABG32451 Hepatitis
13	281	85.9	3010	ABG32455	ABG32455 Hepatitis
14	281	85.9	3010	ABG32457	ABG32457 Hepatitis
15	281	85.9	3010	ABG32460	ABG32460 Hepatitis
16	281	85.9	3010	ABG32453	ABG32453 Hepatitis
17	281	85.9	3010	ABG32461	ABG32461 Hepatitis
18	281	85.9	3010	ABG32454	ABG32454 Hepatitis
19	281	85.9	3010	ABG32452	ABG32452 Hepatitis
20	281	85.9	3011	ABG32456	ABG32456 Hepatitis
21	279	85.3	3010	AAR30616	Aar30616 Polyprot
22	278	85.0	3010	AAE20477	AAE20477 HCV-S1 fu
23	277	84.7	3011	AAR34468	Aar34468 Encoded b
24	275	84.1	258	AAW41735	Aaw41735 Hepatitis
25	275	84.1	259	AAR25857	Aar25857 HCV poly

26	275	84.1	480	2	AAR34000
27	275	84.1	980	2	AAR53921
28	275	84.1	1010	2	AAR88311
29	275	84.1	3010	2	AAR68622
30	275	84.1	3010	2	AAR68864
31	275	84.1	3010	2	AAR82694
32	275	84.1	3010	7	ADF88597
33	274	83.8	283	2	AAR29853
34	274	83.8	283	2	AAR29851
35	274	83.8	845	2	AAW68466
36	274	83.8	1031	2	AAR54067
37	274	83.8	1031	2	AAR96362
38	274	83.8	1188	2	AAR29870
39	274	83.8	3010	2	AAR34580
40	273	83.5	1051	2	AAR54066
41	273	83.5	1051	2	AAR98361
42	273	83.5	3010	2	AAW98022
43	273	83.5	3010	4	AAW59174
44	273	83.5	3010	4	AAW31170
45	273	83.5	3010	8	ADO36227

ALIGNMENTS

RESULT 1	
ID	AAR29852 standard; protein; 283 AA.
XX	
AC	AAR29852;
XX	
DT	25-MAR-2003 (revised)
DT	26-APR-1993 (first entry)
XX	
DE	HCV NS2-NS4 peptide WX25-2.
XX	
KW	Clone; polypeptide; NS2-NS4; Hepatitis C; virus; HCV; serum; HC;
KW	transcriptase; cDNA; primer; allele.
XX	
OS	Hepatitis C virus.
XX	
PN	EP518313-A2.
XX	
PD	16-DEC-1992.
XX	
PF	11-JUN-1992; 92EP-00109812.
XX	
PR	11-JUN-1991; 91JP-00139268.
PR	12-JUL-1991; 91JP-00172794.
PR	07-OCT-1991; 91JP-00287008.
PR	16-DEC-1991; 91JP-00332329.
PR	20-APR-1992; 92JP-00099957.
PA	(MITU) MITSUBISHI KASEI CORP.
XX	
PI	Seki M, Honda Y, Takahashi K, Murakami T, Teranishi Y, Hayashi N;
XX	
DR	WPI; 1992-417213/51.
DR	N-PSDB; AAQ32483.
XX	
PT	New hepatitis C virus gene and its encoded protein - used for diagnosing
PT	and vaccinating against hepatitis C virus infections.
XX	
PS	Disclosure; Page 147-49; 305PP; English.
XX	
CC	The sequences given in AAR29852-70 are encoded by various clones which
CC	were used in the isolation of the NS2-NS4 regions of the Hepatitis C
CC	virus (HCV) gene of the invention (see also AAR29660, AAR29559-60 and
CC	AAR29843-51). These RNA sequences were isolated from the serum of a
CC	patient suffering from hepatitis C (HC). The isolated RNA sequences were
CC	converted into cDNA using transcriptase in the presence of one of the
CC	primer sequences given in AAQ32578-79. The sequences were then amplified
CC	using primer pairs. The cDNA sequences isolated represent different

CC alleles of the same region of the HCV gene. Sequence comparisons of these
 CC clones showed that it is possible for a patient to carry more than one
 CC HCV strain at one time. See also AAQ32436. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX

SQ Sequence 283 AA;

Query Match 86.5%; Score 283; DB 2; Length 283;
 Best Local Similarity 85.7%; Pred. No. 9.6e-29;
 Matches 54; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 ALENLVNNAASAGHGLIMPLVFCAMVYKGRLVGATYSLGLMPLLLLLALPQR 60
 DB 16 ALENLVNNAASAGHGLISFLVFCAMWYIKGRLVGATYALYGVWPLLLLLALPPR 75

QY 61 AYA 63
 DB 76 AYA 78

RESULT 2

AAAR34002
 ID AAR34002 standard; protein; 480 AA.

AC AAR34002;

DT 25-MAR-2003 (revised)
 DT 26-JUL-1993 (first entry)

DE BK E2/NS1 protein.

KW Polymerase chain reaction; PCR; amplify; primer; hepatitis C virus; HCV;
 KW asymptomatic; chronically infected; epitope; viral isolate; domain;
 KW immunological; cross-reactive; envelope protein; vaccine;
 KW gp53 (BVDV)/gp55; hog cholera virus; pestivirus; NS1; flavivirus.

OS Synthetic.

PN WO9306126-A1.

PD 01-APR-1993.

PF 11-SEP-1992; 92MO-US007683.

PR 13-SEP-1991; 91US-00759575.

PA (CHIR) CHIRON CORP.

PI Weiner AJ, Houghton M;

DR WPI; 1993-117468/14.

PT Immuno-reactive hepatitis C virus polypeptide compans. - contg. at least
 PT 2 sequences from the first variable domain of distinct HCV isolates.

PS Disclosure; Fig 3; 106pp; English.

CC The sequences given in AAR33992-002 represent a portion of the E2/NS1
 CC protein encoded by group I and group II HCV isolates, from amino acid 370
 CC -850. E2/NS1 are viral envelope proteins and are of immunogenic interest.
 CC E2/NS1 contains an N-terminal hypervariable domain of about 30 amino
 CC acids which shows large variation between nearly all isolates. This is an
 CC important immunoreactive domain. This putative envelope glycoprotein
 CC E2/NS1 may correspond to the gp53(BVDV)/gp55 (hog cholera virus) envelope
 CC polypeptide of the pestiviruses and the NS1 of the flaviviruses, both of
 CC which confer protective immunity in hosts vaccinated with these
 CC polypeptides. It has been discovered that a number of important HCV
 CC epitopes vary among viral isolates and that these epitopes can be mapped
 CC to specific domains. This meant that immunologically cross-reactive
 CC polypeptides which focus on variable rather than constant domains can be
 CC produced. See also AAQ39134-48 and AAR33982-91. (Updated on 25-MAR-2003
 CC to correct PN field.)
 XX

SQ Sequence 480 AA;

Query Match 86.5%; Score 283; DB 2; Length 480;
 Best Local Similarity 85.7%; Pred. No. 1.8e-28;
 Matches 54; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 ALENLVNNAASAGHGLIMPLVFCAMVYKGRLVGATYSLGLMPLLLLLALPQR 60
 DB 378 ALENLVNNSASVAGHGLISFLVFCAMWYIKGRLVGATYALYGVWPLLLLLALPPR 437

QY 61 AYA 63
 DB 438 AYA 440

RESULT 3

AAAR20111
 ID AAR20111 standard; protein; 3010 AA.

AC AAR20111;

DT 25-MAR-2003 (revised)
 DT 01-MAY-1992 (first entry)

DE Non-A, non-B viral genome product.

KW NANBV; vaccine; immunodiagnosis; antigen; antibody.

OS Non-A.

XX non-B hepatitis virus.

FH Key Location/Qualifiers

FT Protein

FT Protein

FT Protein

FT Protein

FT Protein

FT Protein

FT Protein

FT Protein

FT Protein

FT Protein

FT Protein

FT Protein

FT Protein

FT Protein

FT Protein

FT Protein

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FT Protein

FT Protein

FT Protein

FT Protein

PT Non-A, non-B hepatitis virus (NANBV) particles - as vaccine, immuno-
PT diagnostics and screening agents for NANBV, and to remove NANBV from
PT blood.
XX
XX Disclosure; Fig 2; 89pp; English.
PS
XX The sequence (SEQ ID NO 1) was deduced from several overlapping from a
CC library prep. from NANBV RNA. Antigenic polypeptides from the sequence
CC can be used as immunoassay reagents, for screening donated blood, and as
CC immunogens for vaccine prodn. Antibodies raised to the peptides can be
CC used in immunoassays to detect or quantify NANBV antigens in liver tissue
CC and blood. Preferred poly- peptides include residues 1-30, -115, or 2012;
CC 47-77; 116-191; 192-207 or -298; 230-238 or -263; 287-300; 293-330; 390-
CC 729; 730-1005; 1006-1614; 1384-1414; 1615-1862; 1737-1767; 1863-2012;
CC and 2013-3010. The sequence is also disclosed in EP-464287 (SEQ ID NO 1).
CC See AAR20091 for details of this specification. (Updated on 25-MAR-2003
CC to correct PD field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 3010 AA;
SQ

Query Match 86.5%; Score 283; DB 2; Length 3010;
Best Local Similarity 85.7%; Pred. No. 1.4e-27;
Matches 54; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 ALENLVNNAASAGTGILMFLVFCAMVYKGRVPGATYSLLGLMPLLLLLALPQR 60
DB 747 ALENLVNNSASVAGAGILSFVLFPCAMVYKGRVPGATYALYGVWPLLLLLALP 806
OY 61 AYA 63
DB 807 AYA 809

RESULT 4
AAR20091
ID AAR20091 standard; protein; 3010 AA.
XX
XX AAR20091;
AC
DT 25-MAR-2003 (revised)
DT 01-MAY-1992 (first entry)
XX
XX Non-A, non-B viral genome product.
DE
XX NANBV; vaccine; immunodiagnosis; antigen; antibody.
KW
XX Non-A.
OS non-B hepatitis virus.
OS
XX
FH Key Location/Qualifiers
FT 1. .115
FT /label= C
FT /note= "core protein"
FT 116. .191
FT /label= M
FT /note= "matrix protein"
FT 192. .389
FT /label= E
FT /note= "envelope protein"
FT 390. .729
FT /label= NS1
FT 730. .1006
FT /label= NS2
FT 1007. .1614
FT /label= NS3
FT 1615. .1862
FT /label= NS4a
FT 1863. .2012
FT /label= NS4b
FT 2013. .3010
FT Protein
FT
XX EP464287-A.

XX
PD 08-JAN-1992.
XX
XX 28-DEC-1990; 90EP-00314371.
PF
XX 25-JUN-1990; 90JP-00167466.
XX 31-AUG-1990; 90JP-00230921.
PR 09-NOV-1990; 90JP-00305605.
PR 17-JUN-1991; 91EP-00401604.
XX
XX (OSAU) UNIV OSAKA.
PA
XX WPI; 1992-009617/02.
DR N-PSDB; AAQ21829.
PT New DNA from non-A, non-B hepatitis virus - and derived antigenic
PT polypeptide(s) useful for diagnostics, blood screening and in vaccines.
XX
XX Claim 3; Fig 2; 89pp; English.
XX
XX The sequence was deduced from several overlapping "BK" cDNA clones obt.
CC by "gene walking" using a cDNA clone isolated from a library prep. from
CC NANBV RNA. Antigenic polypeptides from the sequence can be used as
CC immunoassay reagents, for screening donated blood, and as immunogens for
CC vaccine prodn. Antibodies raised to the peptides can be used in
CC immunoassays to detect or quantify NANBV antigens in liver tissue and
CC blood. Preferred polypeptides are include residues 1-30, -115, or 2012;
CC 47-77; 116-191; 192-207 or -298; 230-238 or -263; 287-300; 293-330; 390-
CC 729; 730-1005; 1006-1614; 1384-1414; 1615-1862; 1737-1767; 1863-2012;
CC and 2013-3010. The sequence is also disclosed in EP-463848 (SEQ ID NO 1)
CC in which a virus particle contg. antigens encoded by the sequence is
CC claimed. See AAR20111 for details of this specification. (Updated on 25-
CC MAR-2003 to correct PA field.)
XX
XX Sequence 3010 AA;
SQ

Query Match 86.5%; Score 283; DB 2; Length 3010;
Best Local Similarity 85.7%; Pred. No. 1.4e-27;
Matches 54; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 ALENLVNNAASAGTGILMFLVFCAMVYKGRVPGATYSLLGLMPLLLLLALPQR 60
DB 747 ALENLVNNSASVAGAGILSFVLFPCAMVYKGRVPGATYALYGVWPLLLLLALP 806
OY 61 AYA 63
DB 807 AYA 809

RESULT 5
AAV06423
ID AAV06423 standard; protein; 3010 AA.
XX
XX AAV06423;
AC
DT 20-MAR-2003 (revised)
DT 27-SEP-1999 (first entry)
XX
XX Non-A, non-B hepatitis virus polypeptide.
DE
XX Non-A, non-B hepatitis B virus; NANBV; antigen; infection; diagnosis;
KW vaccine.
KW
XX Non-A.
OS non-B hepatitis virus.
OS
XX
FH Key Location/Qualifiers
FT 1. .115
FT /note= "core protein"
FT 116. .191
FT /note= "matrix protein"
FT 192. .389
FT Protein
FT
XX

```

FT Protein 390..729
FT /note= "NS1 protein"
FT Protein 730..1006
FT /note= "NS2 protein"
FT Protein 1007..1615
FT /note= "NS3 protein"
FT Protein 1616..1862
FT /note= "NS4a protein"
FT Protein 1863..2013
FT /note= "NS4b protein"
FT Protein 2014..3010
FT /note= "NS5 protein"
XX
XX EP933426-A1.
XX
XX PD 04-AUG-1999.
XX
XX PF 28-DEC-1990; 99EP-00106005.
XX
XX PR 25-JUN-1990; 90JP-00167466.
XX PR 31-AUG-1990; 90JP-00230921.
XX PR 09-NOV-1990; 90JP-00305605.
XX PR 28-DEC-1990; 90EP-00314371.
XX
XX (OSAU ) UNITV OSAKA.
XX
XX PI Okayama H, Fuke I, Mori C, Takamizawa A, Yoshida I;
XX
XX DR WPI; 1999-407152/35.
XX DR N-PSDB; AAX59394.
XX
XX PT New hepatitis virus polypeptides, useful for diagnosing and treating
XX PT hepatitis infections.
XX
XX PS Claim 2; Fig 2(1) - (16); 56pp; English.
XX
CC This sequence represents the non-A, non-B hepatitis virus (NANBV)
CC polypeptide, as predicted from cDNA (see AAX59394) containing the entire
CC open reading frame of the NANBV genome. To obtain this cDNA, NANBV RNAs
CC were extracted directly from NANBV particles contained in whole blood of
CC a patient having NANB hepatitis, or from a resected liver of a patient
CC having NANB hepatitis and liver cancer. The RNA was then converted to
CC double-stranded cDNA. A cDNA library was produced and screened using
CC serum from a convalescent patient having acute NANB hepatitis and serum
CC from a patient having chronic NANB hepatitis. The isolated cDNA allows
CC recombinant production of NANBV antigen polypeptides in microbial or
CC eukaryotic cell culture. The method provides the safe production of NANBV
CC antigens with high purity on a large scale at low cost without the
CC biohazard associated with multiplying virus in animals. Claimed NANBV
CC nucleotide sequences are useful for the recombinant production of
CC polypeptides useful as antigens for vaccines, and as diagnostic reagents.
CC (Updated on 20-MAR-2003 to correct PF field.) (Updated on 20-MAR-2003 to
CC correct PR field.)
XX
XX SQ Sequence 3010 AA;
XX
Query Match 86.5%; Score 283; DB 2; Length 3010;
Best Local Similarity 85.7%; Pred. No. 1.4e-27;
Matches 54; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
XX
OY 1 ALENLVNNAASAGTHGILMFLVFCAMVYKGRVPGATYSLLGLMPLLLLLALPPR 60
DB 747 ALENLVNNAASVAGAHGILSLVFCAMVYKGRVPGATYALVGVMPPLLLLLALPPR 806
OY 61 AYA 63
DB 807 AYA 809
XX
RESULT 6
ADJ82984
ID ADJ82984 standard; protein; 1026 AA.
XX

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AC ADJ82984;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX Adenovector construct HCV C-E1-E2-P7-NS2 protein sequence.
XX
XX DE Adenovirus construct; vector; hepatitis C virus; viral particle; HCV;
XX HCV infection.
XX
XX OS Synthetic.
XX
XX PN WO2004005524-A1.
XX
XX PD 15-JAN-2004.
XX
XX PF 27-JUN-2003; 2003WO-US020409.
XX
XX PR 02-JUL-2002; 2002US-0393167P.
XX
XX PA (MERI ) MERCK & CO INC.
XX
XX PI Ludmerer SW, Flores OA, Graham D, Wolanski BS;
XX DR WPI; 2004-091376/09.
XX DR N-PSDB; ADJ82983.
XX
XX PT Producing hepatitis C virus (HCV) particles comprises incubating Vero
XX PT cells containing a recombinant nucleic acid that comprises an expression
XX PT cassette encoding for at least a HCV C-E1-E2-P7-NS2 sequence.
XX
XX PS Disclosure; Page 37-39; 53pp; English.
XX
CC The present invention relates to a method of producing hepatitis C virus
CC (HCV) particles by incubating Vero cells containing a recombinant nucleic
CC acid that comprises an expression cassette encoding for at least a HCV C-
CC E1-E2-P7-NS2 sequence under conditions suitable for producing the HCV
CC particles. The method is useful for making hepatitis C virus (HCV)
CC particles and measuring the ability of a compound to inhibit HCV particle
CC formation or function. The HCV particles are useful as source materials
CC for obtaining HCV antibodies recognizing a native particle form, and for
CC evaluating the ability of a compound to inhibit particle function or
CC infectivity. The present sequence is a protein encoded by an adenovector
CC construct designated HCV C-E1-E2-P7-NS2 used to demonstrate the method of
CC the invention.
XX
XX SQ Sequence 1026 AA;
XX
Query Match 85.9%; Score 281; DB 8; Length 1026;
Best Local Similarity 85.7%; Pred. No. 7.7e-28;
Matches 54; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
XX
OY 1 ALENLVNNAASAGTHGILMFLVFCAMVYKGRVPGATYSLLGLMPLLLLLALPPR 60
DB 747 ALENLVNNAASVAGAHGILSLVFCAMVYKGRVPGATYALVGVMPPLLLLLALPPR 806
OY 61 AYA 63
DB 807 AYA 809
XX
RESULT 7
AAJ70064
ID AAJ70064 standard; protein; 2307 AA.
XX
XX AC AAJ70064;
XX
XX DT 12-SEP-2003 (revised)
XX DT 05-JUN-2000 (first entry)
XX
XX DE Recombinant fusion pHCAP-1 polypeptide.
XX
XX KM Recombinant plasmid; pHCAP; Hepatitis C virus; HCV; reporter gene;
XX KM NS3 protease; inhibitor; recombinant viral vector; RVV; HCV infection;
XX

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KM		secreted alkaline phosphatase; SEAP; serine protease; treatment;
KW		recombinant vaccinia virus.
XX		Hepatitis C virus.
OS		Vaccinia virus.
OS		Enterobacteria phage T7.
OS		Homo sapiens.
OS		Chimeric.
XX		
FH	Key	Location/Qualifiers
FT	Region	1..92
PT		/label= pHCAP-1_polypeptide_fragment_1
FT	Region	93..1784
PT		/label= pHCAP-1_polypeptide_fragment_2
FT	Region	93..98
PT		/note= "Additional residues resulting from subcloning of HCV/SEAP fragment"
FT	Domain	100..390
FT		/label= E2/NS2_domain
FT		/note= "Hepatitis C virus non-structural domain"
FT	Domain	391..1028
PT		/label= NS3_domain
FT		/note= "Hepatitis C virus non-structural domain containing serine protease and helicase enzymes"
FT	Cleavage-site	1019..1038
PT		/label= NS3/NS4A_cleavage site
FT	Domain	1029..1082
PT		/label= NS4A_domain
FT		/note= "Hepatitis C virus non-structural domain"
FT	Cleavage-site	1076..1092
PT		/label= NS4A/NS4B_cleavage site
FT	Domain	1083..1257
PT		/label= NS4B_domain
FT		/note= "Hepatitis C virus non-structural domain"
FT	Cleavage-site	1259..1278
PT		/label= NS5A/NS5B_cleavage site
FT	Protein	1282..1784
PT		/label= Secreted alkaline phosphatase protein
FT		/note= "Secreted human placental SEAP"
FT	Region	1785..1936
PT		/label= pHCAP-1_polypeptide_fragment_3
FT	Region	1937..2021
PT		/label= pHCAP-1_polypeptide_fragment_4
FT	Region	2022..2307
PT		/label= pHCAP-1_polypeptide_fragment_5
PN		M0200008469-A1.
PD		
PD		17-FEB-2000.
XX		
PF	02-AUG-1999;	99MO-US017440.
XX		
PR	05-AUG-1998;	98US-00128611.
PR	08-MAR-1999;	99US-00263933.
XX		
PA	(AGOU-) AGOURN PHARM INC.	
XX		
PI	Potts KE, Jackson RL, Patrick AK;	
XX		
DR	WPI; 2000-224057/19.	
DR	N-PSDB; AAZ51002.	
XX		
PT		Assessing compounds which augment or inhibit Hepatitis C virus NS3 protease, useful particularly for identifying inhibitors which can be used for treating Hepatitis C virus infections.
XX		
PS	Claim 39; Page 70-78; 153pp; English.	
CC		The patent discloses a reporter gene system for use in a cell-based assessment of inhibitors of Hepatitis C virus (HCV) NS3 protease, using a recombinant viral vector (RVV), that expresses a secreted human placental alkaline phosphatase (SEAP) reporter gene polypeptide, under the control of bacteriophage T7 promoter. The viral vector has been engineered to

	CC	expresses polyprotein, that includes NS3 HCV serine protease and the
	CC	human SEAP gene. This assay system is useful for in vitro screening of
	CC	potential protease inhibitors useful in the treatment of HCV infections
	CC	and used to evaluate potent NS3 inhibitors, by monitoring the effect of
	CC	increasing drug concentration on SEAP activity. NS3 inhibition is
	CC	detected as a decrease in SEAP activity. The present sequence is the
	CC	recombinant fusion protein, encoded by the RVV pHCAP-1, comprising five
	CC	segments and the active NS2 and NS3 protease polyproteins, fused with the
	CC	SEAP reporter protein. The plasmid is constructed using the pTM3 vector
	CC	and has been used to generate recombinant vaccinia viruses. (Updated on
	CC	12-SEP-2003 to standardise OS field)
	XX	
SQ	Sequence 2307 AA:	
OY	Query Match	.85.9%; Score 261; DB 3; Length 2307;
Dd	Best Local Similarity	85.7% ; Pred. No. 1.9e+27;
	Matches 54; Conservative 3; Mismatches 6; Indels 0; Gaps 0;	
Oy	1 ALENLVLTNMAAGTGTGILMELTFPCAWVRKGLVPATYSLGLMLTLITLAIPQR 60 : - 118 ALENVLTNMAASVGAHGISLFVFPCAAYIKGRLLVPGAAYALYGWPLDHLAIPR 177	
Oy	61 AYA 63 Db 178 AYA 180	
RESULT 8		
ID	AAY70065 standard; protein; 2307 AA.	
AC	AAY70065;	
XX		
DT	12-SEP-2003 (revised)	
DT	05-JUN-2000 (first entry)	
xx		
DE	Recombinant fusion pHCAP-3 polyprotein.	
XX		
KX	Recombinant plasmid; pHCAP; Hepatitis C virus; HCV; reporter gene;	
KM	NS3 protease; inhibitor; recombinant viral vector; RVV; HCV infection;	
KW	secreted alkaline phosphatase; SEAP; serine protease; treatment;	
KM	recombinant vaccinia virus.	
XX		
OS	Hepatitis C virus.	
OS	Vaccinia virus.	
OS	Enterobacteria phage T7.	
OS	Homo sapiens.	
OS	Chimeric.	
XX		
FH	Key	
FT	Region	Location/Qualifiers
FT	/label= pHCAP-1_polyprotein_fragment_1	1..92
FT	/label= NS3_NS4A_cleavage site	93..1784
FT	/label= pHCAP-1_polyprotein_fragment_2	93..98
FT	/note= "Additional residues resulting from subcloning of	
FT	HCV/SEAP fragment"	100..390
FT	/label= E2/NS2 domain	
FT	/note= "Hepatitis C virus non-structural domain"	391..1028
FT	/label= NS3_domain	
FT	/note= "Hepatitis C virus non-structural domain	
FT	containing serine protease and helicase enzymes"	
Misc-difference	56 /note= "Wild type catalytic Ser replaced with Ala, to	
FT	Inactivate NS3 protease"	
FT	1019..1038	
FT	/label= NS3/NS4A_cleavage site	
FT	1029..1082	
FT	/label= NS4A domain	
FT	/note= "Hepatitis C virus non-structural domain"	
Cleavage-site	1076..1092	

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FT      Domain                               /label= NS4A/NS4B_cleavage site
XX      1083..1257
FT      /label= NS4B_domain
XX      /note= "Hepatitis C virus non-structural domain"
FT      Cleavage-site                       /label= NS5A/NS5B_cleavage site
XX      1259..1278
FT      /label= NS5A/NS5B_cleavage site
XX      1282..1784
FT      Protein                             /label= Secreted alkaline phosphatase protein
XX      /note= "Secreted human placental SEAP"
FT      Region                             /label= NS5A/NS5B_cleavage site
XX      1785..1936
FT      /label= NS5A/NS5B_cleavage site
XX      1937..2021
FT      /label= NS5A/NS5B_cleavage site
XX      2022..2307
FT      Region                             /label= NS5A/NS5B_cleavage site
XX      /label= NS5A/NS5B_cleavage site
XX      WO200008469-A1.
XX      17-FEB-2000.
XX      02-AUG-1999; 99WO-US017440.
XX      05-AUG-1998; 98US-00129611.
XX      08-MAR-1999; 99US-00263933.
XX      (AGOU-) AGOURN PHARM INC.
XX      Potter KE, Jackson RL, Patrick AK;
XX      MPI; 2000-224057/19.
XX      N-PSDB; AA251003.
XX      Assessing compounds which augment or inhibit Hepatitis C virus NS3
XX      protease, useful particularly for identifying inhibitors which can be
XX      used for treating Hepatitis C virus infections.
XX      Claim 40; Page 101-108; 153pp; English.
XX      The patent discloses a reporter gene system for use in a cell-based
XX      assessment of inhibitors of Hepatitis C virus (HCV) NS3 protease, using a
XX      recombinant viral vector (RVV), that expresses a secreted human placental
XX      alkaline phosphatase (SEAP) reporter gene polypeptide, under the control
XX      of bacteriophage T7 promoter. The viral vector has been engineered to
XX      express a polypeptide, that includes NS3 HCV serine protease and the
XX      human SEAP gene. This assay system is useful for in vitro screening of
XX      potential protease inhibitors useful in the treatment of HCV infections
XX      and used to evaluate potent NS3 inhibitors, by monitoring the effect of
XX      increasing drug concentration on SEAP activity. NS3 inhibition is
XX      detected as a decrease in SEAP activity. The present sequence is the
XX      recombinant fusion protein, encoded by the RVV pHCAP-3, comprising five
XX      segments and the active NS2 and mutant NS3 protease, fused with the SEAP
XX      reporter protein. The NS3 protease is inactivated by site directed
XX      mutagenesis. The plasmid is constructed using the pTM3 vector and has
XX      been used to generate recombinant vaccinia viruses. (Updated on 12-SEP-
XX      2003 to standardize OS field)
XX      Sequence 2307 AA;
XX      Query Match 85.9%; Score 281; DB 3; Length 2307;
XX      Best Local Similarity 85.7%; Pred. No. 1.9e-27;
XX      Matches 54; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
XX      1 ALENTLVNAAAGTGILMFLVFCAMVYKGRVPGATYSLGLWPLLLLLALPPR 60
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XX      61 AYA 63
XX      |||||
XX      178 AYA 180
XX      |||||
XX      RESULT 9
XX      AAY70066

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ID      AAY70066 standard; protein; 2307 AA.
XX      AAY70066;
XX      12-SEP-2003 (revised)
XX      05-JUN-2000 (first entry)
XX      Recombinant fusion pHCAP-4 polypeptide.
XX      Recombinant plasmid; pHCAP; Hepatitis C virus; HCV; reporter gene;
XX      NS3 protease; inhibitor; recombinant viral vector; RVV; HCV infection;
XX      secreted alkaline phosphatase; SEAP; serine protease; treatment;
XX      recombinant vaccinia virus.
XX      Hepatitis C virus.
XX      Vaccinia virus.
XX      Enterobacteria phage T7.
XX      Homo sapiens.
XX      Chimeric.
XX      Key
XX      Location/Qualifiers
XX      Region
XX      /label= pHCAP-1_polypeptide_fragment_1
XX      93..1784
XX      /label= pHCAP-1_polypeptide_fragment_2
XX      93..98
XX      /note= "Additional residues resulting from subcloning of
XX      HCV/SEAP fragment"
XX      100..390
XX      /label= E2/NS2 domain
XX      /note= "Hepatitis C virus non-structural domain"
XX      364
XX      /note= "Wild type catalytic Cys replaced with Ala, to
XX      inactivate NS2 protease"
XX      391..1028
XX      /label= NS3 domain
XX      /note= "Hepatitis C virus non-structural domain
XX      containing serine protease and helicase enzymes"
XX      536
XX      /note= "Wild type catalytic Ser replaced with Ala, to
XX      inactivate NS3 protease"
XX      1019..1038
XX      /label= NS3/NS4A_cleavage site
XX      1029..1082
XX      /label= NS4A domain
XX      /note= "Hepatitis C virus non-structural domain"
XX      1076..1092
XX      /label= NS4A/NS4B_cleavage site
XX      1083..1257
XX      /label= NS4B domain
XX      /note= "Hepatitis C virus non-structural domain"
XX      1259..1278
XX      /label= NS5A/NS5B_cleavage site
XX      1282..1784
XX      /label= Secreted alkaline phosphatase protein
XX      /note= "Secreted human placental SEAP"
XX      1785..1936
XX      /label= NS5A/NS5B_cleavage site
XX      1937..2021
XX      /label= NS5A/NS5B_cleavage site
XX      2022..2307
XX      /label= pHCAP-1_polypeptide_fragment_5
XX      WO200008469-A1.
XX      17-FEB-2000.
XX      02-AUG-1999; 99WO-US017440.
XX      05-AUG-1998; 98US-00129611.
XX      08-MAR-1999; 99US-00263933.
XX      (AGOU-) AGOURN PHARM INC.

```

XX Potte KE, Jackson RL, Patlick AK;
XX MPI: 2000-224057/19.
DR N-PSDB; AA251004.
XX
PT Assessing compounds which augment or inhibit Hepatitis C virus NS3
PT protease, useful particularly for identifying inhibitors which can be
PT used for treating Hepatitis C virus infections.
XX
PS Claim 41; Page 132-139; 153pp; English.
XX
XX The patent discloses a reporter gene system for use in a cell-based
CC assessment of inhibitors of Hepatitis C virus (HCV) NS3 protease, using a
CC recombinant viral vector (RVV), that expresses a secreted human placental
CC alkaline phosphatase (SEAP) reporter gene polypeptide, under the control
CC of bacteriophage T7 promoter. The viral vector has been engineered to
CC express a polypeptide, that includes NS3 HCV serine protease and the
CC human SEAP gene. This assay system is useful for in vitro screening of
CC potential protease inhibitors useful in the treatment of HCV infections
CC and used to evaluate potent NS3 inhibitors, by monitoring the effect of
CC increasing drug concentration on SEAP activity. NS3 inhibition is
CC detected as a decrease in SEAP activity. The present sequence is the
CC recombinant fusion protein, encoded by the RVV pHCAP-4, comprising five
CC segments and the mutant inactive NS2 and mutant inactive NS3 protease
CC polypeptides, fused with the SEAP reporter protein. The NS2-NS3 domain
CC are inactivated by site directed mutagenesis. The plasmid is constructed,
CC using the pTR3 vector and has been used to generate recombinant vaccinia
CC viruses. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 2307 AA;
XX
Query Match 85.9%; Score 281; DB 3; Length 2307;
Best Local Similarity 85.7%; Pred. No. 1.9e-27;
Matches 54; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
XX
QY 1 ALENLVVINAASAAAGTGTGILFVFCAMVYKGRVPGATYSLLGLPILLILLALPPR 60
DB 118 ALENLVVINAASVAGAGHLSFLVFCAMVYKGRVPGAAVYALGVWPLLILLALPPR 177
XX
QY 61 AYA 63
DB 178 AYA 180
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RESULT 10
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ID ABG32458 standard; protein; 3010 AA.
XX
AC ABG32458;
XX
DT 15-NOV-2002 (first entry)
XX
DE Hepatitis C virus Con 1 isolate polypeptide mutant #7.
XX
XX HCV, Con 1; adaptive mutation; liver failure; cirrhosis; mutant; mutcin;
KM hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;
KM internal ribosome entry site; IRES; NS5A; HCV replication; polypeptide.
XX
OS Hepatitis C virus.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Mlec-difference 2197 /note="wild-type Phe substituted by Ser"
XX
XX WO200259321-A2.
XX
XX 01-AUG-2002.
XX
XX 16-JAN-2002; 2002WO-BP000526.
XX
XX 23-JAN-2001; 2001US-0263479P.
XX
XX

XX (RICE-) IST RICERCHI BIOL MOLECOLARE ANGELETTI.
XX De Francesco R, Migliaccio G, Paonessa G;
XX MPI: 2002-599793/64.
XX
XX
XX New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV
PT NS5 encoding region, or encephalomyocarditis virus (EMCV) internal
PT ribosome entry site (IRES) region, useful in studying HCV replication and
PT expression.
XX
XX Claim 1; Page; 69pp; English.
XX
XX The invention relates to nucleic acid molecules comprising altered HCV
CC NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)
CC internal ribosome entry site (IRES) region coding for one or more NS3,
CC NS5A, or EMCV IRES mutations, respectively. The location of the mutations
CC are detailed in the specification. Also included are (1) an expression
CC vector comprising a nucleotide sequence coding for the altered nucleic
CC acids, which is transcriptionally coupled to an exogenous promoter; (2) a
CC recombinant cell human hepatoma cell comprising the altered nucleic acids
CC; (3) a recombinant cell produced by introducing into a human hepatoma
CC cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus)
CC replicon enhanced cell or which containing a functional HCV replicon; (5)
CC an HCV replicon enhanced cells made in the method; and (6) measuring the
CC ability of a compound to affect HCV activity. The HCV replicons and HCV
CC replicon enhanced cells are useful in studying HCV replication and
CC expression, and HCV and host cell interactions, producing HCV RNA and
CC proteins, and providing a system for measuring the ability of a compound
CC to modulate one or more HCV activities e.g. to discover drugs which may
CC treat HCV mediated diseases such as liver failure, cirrhosis and
CC hepatocellular carcinoma. The present sequence is the HCV replicon Con 1
CC polypeptide (comprising the Core, E1, E2, E3, NS2, NS3, NS4A, NS4B, NS5A
CC and NS5B proteins), NS5A mutant of the invention. Note: The present
CC sequence is not shown in the specification but was created by the indexer
CC using the HCV sequence appearing as ABG32451 and the information in claim
CC 1
XX
SQ Sequence 3010 AA;
XX
Query Match 85.9%; Score 281; DB 5; Length 3010;
Best Local Similarity 85.7%; Pred. No. 2.6e-27;
Matches 54; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
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DB 747 ALENLVVINAASVAGAGHLSFLVFCAMVYKGRVPGAAVYALGVWPLLILLALPPR 806
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QY 61 AYA 63
DB 807 AYA 809
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RESULT 11
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ID ABG32459 standard; protein; 3010 AA.
XX
AC ABG32459;
XX
DT 15-NOV-2002 (first entry)
XX
DE Hepatitis C virus Con 1 isolate polypeptide mutant #8.
XX
XX HCV, Con 1; adaptive mutation; liver failure; cirrhosis; mutant; mutcin;
KM hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;
KM internal ribosome entry site; IRES; NS5A; HCV replication; polypeptide.
XX
OS Hepatitis C virus.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Mlec-difference 2198
XX
XX


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XX Hepatitis C virus Con 1 isolate polypeptide mutant #4.
XX
XX HCV, Con 1; adaptive mutation; liver failure; cirrhosis; mutant; mutein;
XX hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;
XX internal ribosome entry site; IRES; NS5A; HCV replication; polypeptide.
XX
XX Hepatitis C virus.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX MISC-difference 2041 /note= "Wild-type Asn substituted by Thr"
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XX MO200259321-A2.
XX
XX 01-AUG-2002.
XX
XX 16-JAN-2002; 2002WO-EP000526.
XX
XX 23-JAN-2001; 2001US-0263479P.
XX
XX (RICE-) 1ST RICERCHE BIOL MOLECULAIRE ANGELETTI.
XX De Francesco R, Migliaccio G, Paonessa G;
XX
XX WPI, 2002-599793/64.
XX
XX New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV
XX NS5 encoding region, or encephalomyocarditis virus (EMCV) internal
XX ribosome entry site (IRES) region, useful in studying HCV replication and
XX expression.
XX
XX Claim 1, Page: 69pp; English.
XX
XX The invention relates to nucleic acid molecules comprising altered HCV
XX NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)
XX internal ribosome entry site (IRES) region coding for one or more NS3,
XX NS5A, or EMCV IRES mutations, respectively. The location of the mutations
XX are detailed in the specification. Also included are (1) an expression
XX vector comprising a nucleotide sequence coding for the altered nucleic
XX acids, which is transcriptionally coupled to an exogenous promoter; (2) a
XX recombinant cell human hepatoma cell comprising the altered nucleic acids
XX; (3) a recombinant cell produced by introducing into a human hepatoma
XX cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus)
XX replicon enhanced cell or which containing a functional HCV replicon; (5)
XX an HCV replicon enhanced cell made in the method; and (6) measuring the
XX ability of a compound to affect HCV activity. The HCV replicons and HCV
XX replicon enhanced cells are useful in studying HCV replication and
XX expression, and HCV and host cell interactions, producing HCV RNA and
XX proteins, and providing a system for measuring the ability of a compound
XX to modulate one or more HCV activities e.g. to discover drugs which may
XX treat HCV mediated diseases such as liver failure, cirrhosis and
XX hepatocellular carcinoma. The present sequence is the HCV replicon Con 1
XX polypeptide (comprising the Core, E1, E2, P7, NS2, NS3, NS4A, NS4B, NS5A
XX and NS5B proteins), NS5A mutant of the invention. Note: The present
XX sequence is not shown in the specification but was created by the indexer
XX using the HCV sequence appearing as ABG32451 and the information in claim
XX 1
XX
XX Sequence 3010 AA:
XX
XX Query Match 85.9%; Score 281; DB 5; Length 3010;
XX Best Local Similarity 85.7%; Pred. No. 2.6e-27;
XX Matches 54; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
XX
XX 1 ALENNVANAASAGTHGLVFWFPCAAWYKGLVFGATSLGLPVLILLALPQR 60
XX 747 ALENNVANAASVAGAHGLVFLVPCAAWYKGLVFGATSLGLPVLILLALPQR 806
XX
XX 61 AYA 63
XX
XX 807 AYA 809
XX

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ID ABG32457 standard; protein: 3010 AA.
XX
XX ABG32457;
XX
XX 15-NOV-2002 (first entry)
XX
XX Hepatitis C virus Con 1 isolate polypeptide mutant #6.
XX
XX HCV, Con 1; adaptive mutation; liver failure; cirrhosis; mutant; mutein;
XX hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;
XX internal ribosome entry site; IRES; NS5A; HCV replication; polypeptide.
XX
XX Hepatitis C virus.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX MISC-difference 2173 /note= "Wild-type Phe substituted by Ser"
XX
XX MO200259321-A2.
XX
XX 01-AUG-2002.
XX
XX 16-JAN-2002; 2002WO-EP000526.
XX
XX 23-JAN-2001; 2001US-0263479P.
XX
XX (RICE-) 1ST RICERCHE BIOL MOLECULAIRE ANGELETTI.
XX De Francesco R, Migliaccio G, Paonessa G;
XX
XX WPI, 2002-599793/64.
XX
XX New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV
XX NS5 encoding region, or encephalomyocarditis virus (EMCV) internal
XX ribosome entry site (IRES) region, useful in studying HCV replication and
XX expression.
XX
XX Claim 1, Page: 69pp; English.
XX
XX The invention relates to nucleic acid molecules comprising altered HCV
XX NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)
XX internal ribosome entry site (IRES) region coding for one or more NS3,
XX NS5A, or EMCV IRES mutations, respectively. The location of the mutations
XX are detailed in the specification. Also included are (1) an expression
XX vector comprising a nucleotide sequence coding for the altered nucleic
XX acids, which is transcriptionally coupled to an exogenous promoter; (2) a
XX recombinant cell human hepatoma cell comprising the altered nucleic acids
XX; (3) a recombinant cell produced by introducing into a human hepatoma
XX cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus)
XX replicon enhanced cell or which containing a functional HCV replicon; (5)
XX an HCV replicon enhanced cell made in the method; and (6) measuring the
XX ability of a compound to affect HCV activity. The HCV replicons and HCV
XX replicon enhanced cells are useful in studying HCV replication and
XX expression, and HCV and host cell interactions, producing HCV RNA and
XX proteins, and providing a system for measuring the ability of a compound
XX to modulate one or more HCV activities e.g. to discover drugs which may
XX treat HCV mediated diseases such as liver failure, cirrhosis and
XX hepatocellular carcinoma. The present sequence is the HCV replicon Con 1
XX polypeptide (comprising the Core, E1, E2, P7, NS2, NS3, NS4A, NS4B, NS5A
XX and NS5B proteins), NS5A mutant of the invention. Note: The present
XX sequence is not shown in the specification but was created by the indexer
XX using the HCV sequence appearing as ABG32451 and the information in claim
XX 1
XX
XX Sequence 3010 AA:
XX
XX Query Match 85.9%; Score 281; DB 5; Length 3010;
XX Best Local Similarity 85.7%; Pred. No. 2.6e-27;

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GenCore version 5.1.6
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OM protein - protein search, using BW model

Run on: October 4, 2005, 18:52:30 ; Search time 44 Seconds

(without alignment)
106.884 Million cell updates/sec

Title: US-10-669-175-1

Perfect score: 327

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	283	86.5	88	3	US-09-263-933-23
2	283	86.5	88	4	US-09-919-901-23
3	283	86.5	88	4	US-10-191-966-23
4	283	86.5	277	1	US-08-324-977-38
5	283	86.5	277	2	US-08-384-616-38
6	283	86.5	277	2	US-08-904-686A-38
7	283	86.5	277	3	US-09-315-850-38
8	283	86.5	480	1	US-08-440-542-22
9	283	86.5	480	1	US-08-440-542-22
10	283	86.5	480	1	US-08-231-368-22
11	283	86.5	480	1	US-08-440-210-22
12	283	86.5	480	3	US-09-046-604-22
13	283	86.5	2013	2	US-08-324-977-12
14	283	86.5	2013	2	US-08-384-616-12
15	283	86.5	2013	2	US-08-904-686A-12
16	283	86.5	2013	3	US-09-315-850-12
17	283	86.5	2620	2	US-08-324-977-32
18	283	86.5	2620	2	US-08-384-616-32
19	283	86.5	2620	3	US-09-904-686A-32
20	283	86.5	2620	3	US-09-315-850-32
21	283	86.5	2621	2	US-08-324-977-36
22	283	86.5	2621	2	US-08-384-616-36
23	283	86.5	2621	2	US-09-904-686A-36
24	283	86.5	2621	2	US-09-315-850-36
25	283	86.5	3010	1	US-08-324-977-2
26	283	86.5	3010	1	US-08-324-977-14
27	283	86.5	3010	2	US-08-384-616-2

26	283	86.5	3010	2	US-08-384-616-14	Sequence 14, Appl
29	283	86.5	3010	2	US-08-904-686A-2	Sequence 2, Appl
30	283	86.5	3010	2	US-08-904-686A-12	Sequence 14, Appl
31	283	86.5	3010	3	US-09-315-850-2	Sequence 2, Appl
32	283	86.5	3010	3	US-09-315-850-14	Sequence 14, Appl
33	283	86.5	3010	3	US-09-263-933-4	Sequence 4, Appl
34	281	85.9	1692	3	US-09-263-933-11	Sequence 11, Appl
35	281	85.9	1692	3	US-09-263-933-18	Sequence 18, Appl
36	281	85.9	1692	4	US-09-919-901-4	Sequence 4, Appl
37	281	85.9	1692	4	US-09-919-901-11	Sequence 11, Appl
38	281	85.9	1692	4	US-09-919-901-18	Sequence 18, Appl
39	281	85.9	1692	4	US-10-191-966-4	Sequence 4, Appl
40	281	85.9	1692	4	US-10-191-966-11	Sequence 11, Appl
41	281	85.9	1692	4	US-10-191-966-18	Sequence 18, Appl
42	281	85.9	2307	3	US-09-263-933-2	Sequence 2, Appl
43	281	85.9	2307	3	US-09-263-933-9	Sequence 9, Appl
44	281	85.9	2307	3	US-09-263-933-16	Sequence 16, Appl
45	281	85.9	2307	4	US-09-919-901-2	Sequence 2, Appl

ALIGNMENTS

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RESULT 1
US-09-263-933-23
; Sequence 23, Application US/09263933
; Patent No. 6280340
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT FILING DATE: 1999-03-08
; EARLIER APPLICATION NUMBER: 09/129, 611
; EARLIER FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: Fragment of the HCV polypeptide
US-09-263-933-23
Query Match      86.5%; Score 283; DB 3; Length 88;
Best Local Similarity 85.7%; Pred. No. 6.2e-29;
Matches 54; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

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DB      19 ALENLVVYNASVAGTHGILWLFVFCAMWYKGRVLGATYSLLGLWPLLLLLALPQRAYA 78
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      61 AYA 63
      |||
DB      79 AYA 81

RESULT 2
US-09-919-901-23
; Sequence 23, Application US/09919901
; Patent No. 6599738
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A

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1 CURRENT APPLICATION NUMBER: US/09/9219,901
2
3 CURRENT FILING DATE: 2001-08-02
4
5 PRIOR APPLICATION NUMBER: 09/263,933
6
7 PRIOR FILING DATE: 1999-02-08
8
9 PRIOR APPLICATION NUMBER: 09/129,611
10
11 PRIOR FILING DATE: 1998-08-05
12
13 NUMBER OF SEQ ID NOS: 33
14
15 SOFTWARE: PatentIn Ver. 2.0
16
17 SEQ ID NO 23
18
19 LENGTH: 88
20
21 TYPE: PRT
22
23 ORGANISM: Artificial Sequence
24
25 FEATURE:
26
27 OTHER INFORMATION: Description of Artificial Sequence: amino acid
28
29 OTHER INFORMATION: Fragment of the HCV polyprotein
30
31 US-09-919-901-23

```

Query Match	86.5%	Score 283	DB 4	Length 88
Best Local Similarity	85.7%	Pred. No. 6.2e-29		
Matches 54	Conservative	4	Mismatches 5	Indels 0
			Gaps	0

[illegible]

RESULT 3
US-10-191-966-23

```

GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
PRIORITY FILING DATE: 2002-07-10
PRIORITY APPLICATION NUMBER: US/09/263,933
PRIORITY FILING DATE: 1999-03-08
PRIORITY APPLICATION NUMBER: 09/129,611
PRIORITY FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 88
TYPE: PRN
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: amino acid
OTHER INFORMATION: Fragment of the HCV polypeptide
US-10-191-966-23

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Query Match	86.5%	Score 283;	DB 4;	Length 88;
Best Local Similarity	85.7%	Pred. No. 6.2e-29;		
Matches	54;	Conservative	4;	Mismatches 5;
				Indels 0;
				Gaps 0

OY 1 ALENVLVLTNASSAGTHGILMELVFPCAAMYVKGLVPNGATYSLSLGMPLLLLLALPQR 600
| | | | | : | | | | | : | | | | | : | | | | |
DB 19 ALENVLVLTNASSAVGAGHILSLFVFPCAAMYIKKSLVPNGATYALGVMPLLLLLLALPPR 780

QY	61	AYA	63
Db	79	AYA	81

RESULT 4
US-08-324-977-38

Sequence 38, Application US/083224977
Patent No. 5747339
GENERAL INFORMATION:
APPLICANT: OKAYAMA, Hiroto
APPLICANT: FUKU, Isao
APPLICANT: MORI, Chisato
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: YOSHIDA, Iwao
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armstrong, Westerman, Hattori, Mclelland &
ADDRESS: Naughton
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.

```

? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette, 3.5 in, 1.44mb
?
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
?
? SOFTWARE: ASCII
?
? CURRENT APPLICATION NAME:
? APPLICATION NUMBER: US/08/324,977
?
? FILING DATE: 18-OCT-1994
?
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: JP 2-167466
? FILING DATE: 25-JUN-1990
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: JP 2-230921

```

APPLICATION NUMBER: JP 2-305605
 FILING DATE: 09-NOV-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/099,706
 FILING DATE: 30-JUL-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/769,936
 FILING DATE: 02-OCT-1991
 PRIOR APPLICATION NUMBER:
 APPLICATION NUMBER: US 07/635,451
 FILING DATE: 28-DEC-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Stevens-Smith, Theresa M.
 REGISTRATION NUMBER: 36,281
 REFERENCE/DOCKET NUMBER: 900703D
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 655-2930
 TELEFAX: (202) 867-0357
 TELEX: 440142
 INFORMATION FOR SEQ ID NO: 38:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 277 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 IS-08-324-977-38

Query Match	86.5%	Score 283;	DB 1;	Length 277;
Best Local Similarity	85.7%	Pred. No. 2.4e-28;		
Matches 54; Conservative	4;	Mismatches 5;	Indels 0;	Gaps

Oy

1 ALENLVTINASAAGTHGLIMFLVFPCAAMVKGRLVGATYSLGAWLILLTLALPQR 60
||| | : ||| | : ||| | : ||| | :
18 ALENLVLTINSASVAGAHTLSLFVEFCAAMYIKGRVPGATVALYGWPELLLLLLAIPRR 77

QY	61	AYA	63
Db	78	AYA	80

RESULT 5

US-08-384-616-38
Sequence 38, Application US/08384616
Patent No. 5847101
GENERAL INFORMATION:
APPLICANT: OKAYAMA, Hiroko
APPLICANT: FUKE, Isao
APPLICANT: MORI, Chiato
APPLICANT: TAKAMIZAWA, Akahisa
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armstrong, Westerman, Hattori, Mclelland &
ADDRESS: Naughton
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384, 616
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/769, 996
FILING DATE: 02-OCT-1991
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635, 451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Stevens-Smith, Theresa M.
REGISTRATION NUMBER: 36,281
REFERENCE/DOCKET NUMBER: 900703B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
TELEX: 440142
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-384-616-38

Query Match 86.5%; Score 283; DB 2; Length 277;
Best Local Similarity 85.7%; Pred. No. 2.4e-28;
Matches 54; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 ALENLVVINAASAAGTHGLVFWFPCAAWYVKGRLVPGATYSLGLWPLLLLLALPPR 60
DB 18 ALENLVVINSASVAGAGHLSFLVFCAAWYIKGRLVPGATYALYGVWPLLLLLALPPR 77
QY 61 AYA 63
DB 78 AYA 80

RESULT 6

US-08-904-686A-38
Sequence 38, Application US/08904686A
Patent No. 5998130
GENERAL INFORMATION:
APPLICANT: OKAYAMA, Hiroko
APPLICANT: FUKE, Isao
APPLICANT: MORI, Chiato
APPLICANT: TAKAMIZAWA, Akahisa
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armstrong, Westerman, Hattori, Mclelland &
ADDRESS: Naughton
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/904, 686A
FILING DATE: 01-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/324, 977
FILING DATE: 18-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099, 706
FILING DATE: 30-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/769, 996
FILING DATE: 02-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635, 451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Mclelland, Le-Nhung
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 900703G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-904-686A-38

Query Match 86.5%; Score 283; DB 2; Length 277;
Best Local Similarity 85.7%; Pred. No. 2.4e-28;
Matches 54; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 ALENLVVINAASAAGTHGLVFWFPCAAWYVKGRLVPGATYSLGLWPLLLLLALPPR 60
DB 18 ALENLVVINSASVAGAGHLSFLVFCAAWYIKGRLVPGATYALYGVWPLLLLLALPPR 77

Qy 61 AYA 63
|||
Db 78 AYA 80

RESULT 7

US-09-315-850-38
; Sequence 38, Application US/09315850
; Patent No. 6217872
; GENERAL INFORMATION:
; APPLICANT: OKAYAMA, Hiroto
; APPLICANT: FUKE, Isao
; APPLICANT: MORI, Chisato
; APPLICANT: TAKAMIZAWA, Akahisa
; APPLICANT: YOSHIDA, Iwao
; TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
; TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Armstrong, Westerman, Hattori, Mclelland &
; STREET: 1725 K St. N.W. Suite 1000
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 in, 1.44mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,850
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/904,686
; FILING DATE: 01-AUG-1997
; APPLICATION NUMBER: US 08/324,977
; FILING DATE: 18-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-167466
; FILING DATE: 25-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-230921
; FILING DATE: 31-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-305605
; FILING DATE: 09-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/099,706
; FILING DATE: 30-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/769,996
; FILING DATE: 02-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/635,451
; FILING DATE: 28-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Mclelland, Le-Nhung
; REGISTRATION NUMBER: 31,541
; REFERENCE/DOCKET NUMBER: 900703G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 659-2930
; TELEFAX: (202) 887-0357
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-315-850-38

Query Match 86.5%; Score 283; DB 3; Length 277;
Best Local Similarity 85.7%; Pred. No. 2.4e-28;
Matches 54; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ALENLVNPAASPAAGTGLVFWFCAMWYKGLVFGATYSLGLWPLLLALLPQR 60
|||
Db 18 ALENLVNPAASPAAGTGLVFWFCAMWYKGLVFGATYSLGLWPLLLALLPQR 77

Qy 61 AYA 63
|||
Db 78 AYA 80

RESULT 8

US-08-440-103-22
; Sequence 22, Application US/08440103
; Patent No. 5670152
; GENERAL INFORMATION:
; APPLICANT: Weiner, Amy J.
; APPLICANT: Houghton, Michael
; TITLE OF INVENTION: Immunoreactive Polypeptide Compositions
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,103
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,368
; FILING DATE:
; APPLICATION NUMBER: US 07/759,575
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0205.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 480 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-440-103-22

Query Match 86.5%; Score 283; DB 1; Length 480;
Best Local Similarity 85.7%; Pred. No. 4.6e-28;
Matches 54; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ALENLVNPAASPAAGTGLVFWFCAMWYKGLVFGATYSLGLWPLLLALLPQR 60
|||
Db 378 ALENLVNPAASPAAGTGLVFWFCAMWYKGLVFGATYSLGLWPLLLALLPQR 437

Qy 61 AYA 63
|||
Db 438 AYA 440

RESULT 9

US-08-440-542-22
; Sequence 22, Application US/08440542
; Patent No. 5670153
; GENERAL INFORMATION:
; APPLICANT: Weiner, Amy J.
; APPLICANT: Houghton, Michael
; TITLE OF INVENTION: Immunoreactive Polypeptide Compositions
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,542
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,368
; FILING DATE:
; APPLICATION NUMBER: US 07/759,575
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0205.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 480 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-440-542-22
Query Match 86.5%; Score 283; DB 1; Length 480;
Best Local Similarity 85.7%; Pred. No. 4,6e-28;
Matches 54; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 1 ALENLVNANASAGTHGILMTLFFPCAAWYKRLVPGATYSLLGLPLLLLLALPQR 60
DB 378 ALENLVNANASVAGAGHILSLVFPAAWYIKRLVPGATYALGVWPLLLALP 437
QY 61 AYA 63
DB 438 AYA 440
RESULT 10
US-08-231-368-22
; Sequence 22, Application US/08231368
; Patent No. 5756312
; GENERAL INFORMATION:
; APPLICANT: Weiner, Amy J.
; APPLICANT: Houghton, Michael
; TITLE OF INVENTION: Immunoreactive Polypeptide Compositions
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA

ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,368
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,575
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0205.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 480 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-231-368-22
Query Match 86.5%; Score 283; DB 1; Length 480;
Best Local Similarity 85.7%; Pred. No. 4,6e-28;
Matches 54; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 1 ALENLVNANASAGTHGILMTLFFPCAAWYKRLVPGATYSLLGLPLLLLLALPQR 60
DB 378 ALENLVNANASVAGAGHILSLVFPAAWYIKRLVPGATYALGVWPLLLALP 437
QY 61 AYA 63
DB 438 AYA 440
RESULT 11
US-08-440-210-22
; Sequence 22, Application US/08440210
; Patent No. 5768845
; GENERAL INFORMATION:
; APPLICANT: Weiner, Amy J.
; APPLICANT: Houghton, Michael
; TITLE OF INVENTION: Immunoreactive Polypeptide Compositions
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,210
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,368
; FILING DATE:
; APPLICATION NUMBER: US 07/759,575
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:

NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0205.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2708
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-440-210-22

Query Match 86.5%; Score 283; DB 1; Length 480;
Best Local Similarity 85.7%; Pred. No. 4.6e-28;
Matches 54; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 ALENLVNMAASAGTHGLMFLVFCAMVYKGRVPGATYSLLGLMPLLLLLALPQR 60
DB 378 ALENLVNMAASAGTHGLMFLVFCAMVYKGRVPGATYSLLGLMPLLLLLALPQR 437

QY 61 AYA 63
DB 438 AYA 440

RESULT 12
US-09-046-604-22
Sequence 22, Application US/09046604
Patent No. 6303292
GENERAL INFORMATION:
APPLICANT: Weiner, Amy J.
APPLICANT: Houghton, Michael
TITLE OF INVENTION: Immunoreactive polypeptide compositions
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,604
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,368
FILING DATE:
APPLICATION NUMBER: US 07/759,575
FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0205.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2708
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-046-604-22

Query Match 86.5%; Score 283; DB 3; Length 480;
Best Local Similarity 85.7%; Pred. No. 4.6e-28;
Matches 54; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 ALENLVNMAASAGTHGLMFLVFCAMVYKGRVPGATYSLLGLMPLLLLLALPQR 60
DB 378 ALENLVNMAASAGTHGLMFLVFCAMVYKGRVPGATYSLLGLMPLLLLLALPQR 437

QY 61 AYA 63
DB 438 AYA 440

RESULT 13
US-08-324-977-12
Sequence 12, Application US/08324977
Patent No. 5747339
GENERAL INFORMATION:
APPLICANT: OKAYAMA, Hiroto
APPLICANT: FUKU, Isao
APPLICANT: MORI, Chisato
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: YOSHIDA, Iwao
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armstrong, Westerman, Hattori, Mclelland &
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,977
FILING DATE: 18-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Stevens-Smith, Theresa M.
REGISTRATION NUMBER: 36,281
REFERENCE/DOCKET NUMBER: 900703D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
TELEX: 440142
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2013 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-324-977-12

Query Match 86.5%; Score 283; DB 1; Length 2013;
Best Local Similarity 85.7%; Pred. No. 2.5e-27;
Matches 54; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 ALENLVYNASAGTHGILWFVFCAMVYKGRLVGATYSILGLWPLLLLLALPPR 60
DB 747 ALENLVYNASVAGAGHLSFLVFCAMWIKGRLVGATYALGVWPLLLLLALPPR 806

OY 61 AYA 63
DB 807 AYA 809

RESULT 14
US-08-384-616-12
Sequence 12, Application US/08384616
Patent No. 58477101
GENERAL INFORMATION:
APPLICANT: OKAYAMA, Hiroto
APPLICANT: FUKU, Isao
APPLICANT: MORI, Chisato
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: YOSHIDA, Iwao
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armstrong, Westerman, Hattori, Mcleland &
ADDRESS: Naughton
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,616
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-OCT-1991
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Stevens-Smith, Theresa M.
REGISTRATION NUMBER: 36,281
REFERENCE/DOCKET NUMBER: 900703B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
TELEX: 440142
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2013 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-384-616-12

Query Match 86.5%; Score 283; DB 2; Length 2013;
Best Local Similarity 85.7%; Pred. No. 2.5e-27;
Matches 54; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 ALENLVYNASAGTHGILWFVFCAMVYKGRLVGATYSILGLWPLLLLLALPPR 60
DB 747 ALENLVYNASVAGAGHLSFLVFCAMWIKGRLVGATYALGVWPLLLLLALPPR 806

OY 61 AYA 63
DB 807 AYA 809

RESULT 15
US-08-904-686A-12
Sequence 12, Application US/08904686A
Patent No. 598130
GENERAL INFORMATION:
APPLICANT: OKAYAMA, Hiroto
APPLICANT: FUKU, Isao
APPLICANT: MORI, Chisato
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: YOSHIDA, Iwao
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armstrong, Westerman, Hattori, Mcleland &
ADDRESS: Naughton
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/904,686A
FILING DATE: 01-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/324,977
FILING DATE: 18-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mcleland, Je-Nhung
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 900703G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930

; TELEFAX: (202) 887-0357
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2013 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-904-686A-12

Query Match 86.5%; Score 283; DB 2; Length 2013;
Best Local Similarity 85.7%; Pred. No. 2.5e-27;
Matches 54; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ALENLVNINASAGTGHGILWFLVFCQAWYVKGRLVPGATYSLGLMPILLLALPQR 60
Db 747 ALENLVNINASAGTGHGILWFLVFCQAWYVKGRLVPGATYSLGLMPILLLALPQR 806
Qy 61 AYA 63
Db 807 AYA 809

Search completed: October 4, 2005, 18:58:45
Job time : 47 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: October 4, 2005, 18:53:50 ; Search time 165 Seconds
(without alignments)
158,499 Million cell updates/sec

Title: US-10-669-175-1

Perfect score: 327
Sequence: 1 ALENLVVIMASASAGTHGIL.....LLGLWPLLILLALPORAYA 63

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1846076 seqs, 41516000 residues

Total number of hits satisfying chosen parameters: 1846076

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications_AA:*
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19: /cgn2_6/ptodata/2/pubpaa/US11_PUBCOMB.pep:*
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21: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	283	86.5	88	US-09-919-901-23	Sequence 23, Appli
3	283	86.5	88	US-10-191-966-23	Sequence 23, Appli
4	281	85.9	1692	US-09-919-901-4	Sequence 4, Appli
5	281	85.9	1692	US-09-919-901-11	Sequence 11, Appli
6	281	85.9	1692	US-09-919-901-18	Sequence 18, Appli
7	281	85.9	1692	US-10-191-966-4	Sequence 4, Appli
8	281	85.9	1692	US-10-191-966-11	Sequence 11, Appli
9	281	85.9	1692	US-10-191-966-18	Sequence 18, Appli
10	281	85.9	2307	US-09-919-901-2	Sequence 2, Appli
11	281	85.9	2307	US-09-919-901-9	Sequence 9, Appli

12	281	85.9	2307	10	US-09-919-901-16	Sequence 16, Appli
13	281	85.9	2307	14	US-10-191-966-2	Sequence 2, Appli
14	281	85.9	2307	14	US-10-191-966-9	Sequence 9, Appli
15	281	85.9	2307	14	US-10-191-966-16	Sequence 16, Appli
16	281	85.9	3010	15	US-10-467-000-1	Sequence 1, Appli
17	278	85.0	3010	16	US-10-333-449A-34	Sequence 34, Appli
18	272	83.2	315	16	US-10-669-175-4	Sequence 4, Appli
19	272	83.2	315	9	US-09-929-955-5	Sequence 5, Appli
20	272	83.2	315	13	US-10-104-966-5	Sequence 5, Appli
21	272	83.2	315	15	US-10-719-619-5	Sequence 5, Appli
22	272	83.2	315	16	US-10-817-591-5	Sequence 5, Appli
23	272	83.2	3011	9	US-09-929-955-1	Sequence 9, Appli
24	272	83.2	3011	9	US-09-747-419-20	Sequence 20, Appli
25	272	83.2	3011	13	US-10-104-966-1	Sequence 1, Appli
26	272	83.2	3011	13	US-10-104-966-1	Sequence 1, Appli
27	272	83.2	3011	14	US-10-259-775-20	Sequence 20, Appli
28	272	83.2	3011	15	US-10-189-359-14	Sequence 14, Appli
29	272	83.2	3011	15	US-10-226-734-406	Sequence 406, App
30	272	83.2	3011	15	US-10-719-619-1	Sequence 1, Appli
31	272	83.2	3011	16	US-10-817-591-1	Sequence 1, Appli
32	272	83.2	3011	20	US-11-006-313-20	Sequence 20, Appli
33	269	82.3	463	9	US-09-973-025-46	Sequence 46, Appli
34	269	82.3	463	10	US-09-899-303-46	Sequence 46, Appli
35	269	82.3	463	10	US-09-995-808-46	Sequence 46, Appli
36	269	82.3	463	10	US-09-995-860-46	Sequence 46, Appli
37	269	82.3	463	10	US-09-995-791-46	Sequence 46, Appli
38	269	82.3	463	16	US-10-321-798-46	Sequence 46, Appli
39	269	82.3	490	9	US-09-973-025-36	Sequence 36, Appli
40	269	82.3	490	10	US-09-899-303-36	Sequence 36, Appli
41	269	82.3	490	10	US-09-995-808-36	Sequence 36, Appli
42	269	82.3	490	10	US-09-995-860-36	Sequence 36, Appli
43	269	82.3	490	10	US-09-995-791-36	Sequence 36, Appli
44	269	82.3	490	16	US-10-321-798-36	Sequence 36, Appli
45	269	82.3	692	9	US-09-973-025-48	Sequence 48, Appli

ALIGNMENTS

RESULT 1
US-10-669-175-1
; Sequence 1, Application US/10669175
; Publication No. US20040110795A1
; GENERAL INFORMATION:
; APPLICANT: ZITZMAN, NICOLE
; TITLE OF INVENTION: USE OF LINGOSUGAR DERIVATIVES TO INHIBIT ION CHANNEL
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 080618-0304
; CURRENT APPLICATION NUMBER: US/10/669,175
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,560
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: consensus amino acid sequence for HCV p7
US-10-669-175-1

Query Match 100.0%; Score 327, DB 16; Length 63;
Best Local Similarity 100.0%; Pred. No. 4, 7e-31;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALENLVVIMASASAGTHGILVFFCAWYKGRVGGATYSLLGLWPLLILLALPOR 60
DB 1 ALENLVVIMASASAGTHGILVFFCAWYKGRVGGATYSLLGLWPLLILLALPOR 60
QY 61 AYA 63

Db 61 AYA 63

RESULT 2

US-09-919-901-23
; Sequence 23, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
US-09-919-901-23

Query Match 86.5%; Score 283; DB 10; Length 88;
Best Local Similarity 85.7%; Pred. No. 1.1e-25;
Matches 54; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 ALENLVNAAASAGTHGILWLFVFCAMVYKGRVPGATYSLGLWPLLLLLALPOR 60
DB 19 ALENLVNAAASAGTHGILWLFVFCAMVYKGRVPGATYSLGLWPLLLLLALPOR 78
QY 61 AYA 63
DB 79 AYA 81

RESULT 3

US-10-191-966-23
; Sequence 23, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
US-10-191-966-23

Query Match 86.5%; Score 283; DB 14; Length 88;
Best Local Similarity 85.7%; Pred. No. 1.1e-25;
Matches 54; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 ALENLVNAAASAGTHGILWLFVFCAMVYKGRVPGATYSLGLWPLLLLLALPOR 60
DB 19 ALENLVNAAASAGTHGILWLFVFCAMVYKGRVPGATYSLGLWPLLLLLALPOR 78
QY 61 AYA 63
DB 79 AYA 81

RESULT 4

US-09-919-901-4
; Sequence 4, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1692
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-09-919-901-4

Query Match 85.9%; Score 281; DB 10; Length 1692;
Best Local Similarity 85.7%; Pred. No. 3.7e-24;
Matches 54; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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DB 26 ALENLVNAAASAGTHGILWLFVFCAMVYKGRVPGATYSLGLWPLLLLLALPOR 85
QY 61 AYA 63
DB 86 AYA 88

RESULT 5

US-09-919-901-11
; Sequence 11, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11

LENGTH: 1692
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-919-901-11

Query Match 85.9%; Score 281; DB 10; Length 1692;
Best Local Similarity 85.7%; Pred. No. 3.7e-24;
Matches 54; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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DB 26 ALENLVVLMNAAAGTGHILMFLVFCAMVYKGRVPGATYSLLGLMPLLLLLALPQR 85
QY 61 AYA 63
DB 86 AYA 88

RESULT 6

US-09-919-901-18
Sequence 18, Application US/09919901
Publication No. US20030082518A1
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 1692
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-919-901-18

Query Match 85.9%; Score 281; DB 10; Length 1692;
Best Local Similarity 85.7%; Pred. No. 3.7e-24;
Matches 54; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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DB 26 ALENLVVLMNAAAGTGHILMFLVFCAMVYKGRVPGATYSLLGLMPLLLLLALPQR 85
QY 61 AYA 63
DB 86 AYA 88

RESULT 7

US-10-191-966-4
Sequence 4, Application US/10191966
Publication No. US20030175692A1
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10

PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 1692
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-10-191-966-4

Query Match 85.9%; Score 281; DB 14; Length 1692;
Best Local Similarity 85.7%; Pred. No. 3.7e-24;
Matches 54; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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DB 26 ALENLVVLMNAAAGTGHILMFLVFCAMVYKGRVPGATYSLLGLMPLLLLLALPQR 85
QY 61 AYA 63
DB 86 AYA 88

RESULT 8

US-10-191-966-11
Sequence 11, Application US/10191966
Publication No. US20030175692A1
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 1692
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-10-191-966-11

Query Match 85.9%; Score 281; DB 14; Length 1692;
Best Local Similarity 85.7%; Pred. No. 3.7e-24;
Matches 54; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 ALENLVVLMNAAAGTGHILMFLVFCAMVYKGRVPGATYSLLGLMPLLLLLALPQR 60
DB 26 ALENLVVLMNAAAGTGHILMFLVFCAMVYKGRVPGATYSLLGLMPLLLLLALPQR 85
QY 61 AYA 63
DB 86 AYA 88

RESULT 9

US-10-191-966-18
Sequence 18, Application US/10191966
Publication No. US20030175692A1
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.

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; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-10-191-966-18
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Query Match      85.9%; Score 281; DB 14; Length 1692;
Best Local Similarity 85.7%; Pred. No. 3, 7e-24;
Matches 54; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
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        |||||
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```

DB      61 AYA 63
        |||
        86 AYA 88
```

```

RESULT 10
US-09-919-901-2
; Sequence 2, Application US/09/19901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potte, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2307
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-919-901-2
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Query Match      85.9%; Score 281; DB 10; Length 2307;
Best Local Similarity 85.7%; Pred. No. 5, 1e-24;
Matches 54; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
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```

QY      1 ALENLVINAASAGTGTGILWFLVFPCAAMYVKGRLVPGATYSLGLWPLLLLLALPQR 60
        |||||
        118 ALENLVINAASVAGAHGILSFVFCAMWIKGRLVGAAYALGVWPLLLLLALPQR 177
        |||||
```

```

DB      61 AYA 63
        |||
        178 AYA 180
```

```

RESULT 11
US-09-919-901-9
; Sequence 9, Application US/09/19901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potte, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-919-901-9
```

```

Query Match      85.9%; Score 281; DB 10; Length 2307;
Best Local Similarity 85.7%; Pred. No. 5, 1e-24;
Matches 54; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
```

```

QY      1 ALENLVINAASAGTGTGILWFLVFPCAAMYVKGRLVPGATYSLGLWPLLLLLALPQR 60
        |||||
        118 ALENLVINAASVAGAHGILSFVFCAMWIKGRLVGAAYALGVWPLLLLLALPQR 177
        |||||
```

```

DB      61 AYA 63
        |||
        178 AYA 180
```

```

RESULT 12
US-09-919-901-16
; Sequence 16, Application US/09/19901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potte, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-919-901-16
```

```

Query Match      85.9%; Score 281; DB 10; Length 2307;
Best Local Similarity 85.7%; Pred. No. 5, 1e-24;
Matches 54; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
```

```

QY      1 ALENLVINAASAGTGTGILWFLVFPCAAMYVKGRLVPGATYSLGLWPLLLLLALPQR 60
```

Db 118 ALENLVVNAASVAGAGHILSFVFCAMWYIKGRLVGGAAYALYGVWPLLLLLLALPPR 177
Qy 61 AYA 63
Db 178 AYA 180

RESULT 13

US-10-191-966-2
; Sequence 2, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Poter, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-2

Query Match 85.9%; Score 281; DB 14; Length 2307;
Best Local Similarity 85.7%; Pred. No. 5.1e-24;
Matches 54; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ALENLVVNAASVAGAGHILSFVFCAMWYIKGRLVGGAAYALYGVWPLLLLLLALPPR 60
Db 118 ALENLVVNAASVAGAGHILSFVFCAMWYIKGRLVGGAAYALYGVWPLLLLLLALPPR 177
Qy 61 AYA 63
Db 178 AYA 180

RESULT 14

US-10-191-966-9
; Sequence 9, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Poter, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :

OTHER INFORMATION: :

US-10-191-966-9

Query Match 85.9%; Score 281; DB 14; Length 2307;
Best Local Similarity 85.7%; Pred. No. 5.1e-24;
Matches 54; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ALENLVVNAASVAGAGHILSFVFCAMWYIKGRLVGGAAYALYGVWPLLLLLLALPPR 60
Db 118 ALENLVVNAASVAGAGHILSFVFCAMWYIKGRLVGGAAYALYGVWPLLLLLLALPPR 177
Qy 61 AYA 63
Db 178 AYA 180

RESULT 15

US-10-191-966-16
; Sequence 16, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Poter, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: :
US-10-191-966-16

Query Match 85.9%; Score 281; DB 14; Length 2307;
Best Local Similarity 85.7%; Pred. No. 5.1e-24;
Matches 54; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ALENLVVNAASVAGAGHILSFVFCAMWYIKGRLVGGAAYALYGVWPLLLLLLALPPR 60
Db 118 ALENLVVNAASVAGAGHILSFVFCAMWYIKGRLVGGAAYALYGVWPLLLLLLALPPR 177
Qy 61 AYA 63
Db 178 AYA 180

Search completed: October 4, 2005, 19:01:35
Job time : 166 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2005, 18:46:50 ; Search time 14 Seconds
(without alignments)
432.975 Million cell updates/sec

Title: US-10-669-175-1

Perfect score: 327

Sequence: 1 ALENLVNNAASAACTGIL.....LLGLWPLLLALLPQRAYA 63

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR 79:*

1: Pf1:*

2: Pf2:*

3: Pf3:*

4: Pf4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	283	86.5	3010	1 GNMVTC	genome polypeptide
2	277	84.7	3010	1 S18030	genome polypeptide
3	275	84.1	3010	1 GNMVCH	genome polypeptide
4	272	83.2	3011	1 GNMVCH	genome polypeptide
5	271	82.9	3010	1 A45573	genome polypeptide
6	265	82.9	3010	1 GNMVTC	genome polypeptide
7	265	81.0	3011	1 GNMVTC	genome polypeptide
8	264	80.7	3011	1 S40770	genome polypeptide
9	234	71.6	3033	1 GNMVJ8	genome polypeptide
10	227	69.4	3033	1 J01303	genome polypeptide
11	212	64.8	3014	1 J05620	genome polypeptide
12	166	50.8	782	2 S18032	genome polypeptide
13	164	50.2	782	2 S18032	genome polypeptide
14	161	49.2	782	2 PNO677	hypothetical prote
15	160	48.9	782	2 S18075	genome polypeptide
16	158	48.3	782	2 S18031	genome polypeptide
17	157	20.5	157	2 AC2320	hypothetical prote
18	66	20.2	337	2 S76656	hypothetical prote
19	64.5	19.7	286	2 T04367	plasma membrane in
20	64	19.6	400	2 S32804	beta-3-adrenergic
21	63.5	19.4	402	2 A75417	hypothetical prote
22	63.5	19.4	405	2 S65459	beta-3-adrenergic
23	63.5	19.4	420	2 S44900	ZK652.10 protein -
24	63.5	19.4	568	2 S44742	C02C2.4 protein -
25	63	19.3	285	2 AE3024	hypothetical prote
26	63	19.3	317	2 D98260	inner membrane pro
27	63	19.3	366	2 G82069	conserved hypothet
28	61.5	18.8	369	2 S73116	com3 protein - My
29	60.5	18.5	408	1 ORH08E	beta-3-adrenergic

30	60.5	18.5	414	1 ORH083	beta-3-adrenergic
31	60.5	18.5	454	2 AD2460	hypothetical prote
32	60.5	18.5	1337	2 T38949	hypothetical prote
33	60	18.3	285	2 T12342	major intrinsic pr
34	60	18.3	326	2 T30166	hypothetical prote
35	60	18.3	341	2 E96019	probable sugar upt
36	60	18.3	400	2 A41679	beta-3-adrenergic
37	60	18.3	400	2 A53281	hypothetical prote
38	60	18.3	459	2 H83675	hypothetical prote
39	60	18.3	1085	2 H82511	probable hemolysin
40	59.5	18.2	219	2 H75342	conserved hypoch
41	59.5	18.2	283	2 E71310	MFS permease [prol
42	59.5	18.2	516	2 AB3088	proline/betaine tr
43	59.5	18.2	516	2 G98198	probable integral
44	59.5	18.2	665	2 C81439	hypothetical prote
45	59	18.0	133	2 PH0210	

ALIGNMENTS

RESULT 1

GNMVTC
N:Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
protein NS4b; nonstructural protein NS4b; nonstructural protein NS5
C:Species: hepatitis C virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: A38465
R:Takamizawa, A.; Mori, C.; Fuke, I.; Manabe, S.; Murakami, S.; Fujita, J.; Onishi, E.;
J. Virol. 65, 1105-1113, 1991
A>Title: Structure and organization of the hepatitis C virus genome isolated from human
A:Reference number: A38465; MUID:911406598; PMID:1847440
A:Accession: A38465
A:Molecule type: genomic RNA
A:Residues: 1-3010 <TRK>
A:Cross-references: UNIPROT:P26663; EMBL:M58335; NID:G329770; PIDN:AAA72945.1; PID:G3297
C:Superfamily: hepatitis C virus genome polypeptide
C:Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructura
F:2-15/Product: capsid protein C #status predicted <CPC>
F:116-191/Product: envelope protein M #status predicted
F:192-389/Product: major envelope protein E #status predicted <ME>
F:390-729/Product: nonstructural protein NS1 #status predicted <NS1>
F:730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
F:1007-1615/Product: hepacivirin #status predicted <NS3>
F:1230-1337/Region: nucleotide-binding motif A (P-loop)
F:1312-1317/Region: nucleotide-binding motif B
F:1316-1319/Region: DEXH motif
F:1616-1862/Product: nonstructural protein NS4 #status predicted <NS4>
F:1863-2013/Product: nonstructural protein NS4b #status predicted <NS4b>
F:2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F:196,209,234,250,305,325,417,423,430,448,532,540,556,576,623,645,1213,1255,2041,2077,22

Query Match 86.5%; Score 283; DB 1; Length 3010;
Best local similarity 85.7%; Pred. No. 9, 1e-24;
Matches 54; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 ALENLVNNAASAACTGILWPLFPCAAWYKGLVRCATSLGLWPLLLALLPQR 60
DB 747 ALENLVNNAASAACTGILWPLFPCAAWYKGLVRCATSLGLWPLLLALLPQR 806
QY 61 AYA 63
DB 807 AYA 809

RESULT 2
GNMVTC
N:Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
protein NS4b; nonstructural protein NS4b; nonstructural protein NS5
C:Species: hepatitis C virus
A:Variety: isolate JX1

C>Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: F18030; S33570; A68332; S18029
R:Honda, M.; Keneko, S.; Maesashi, U.; Kobayashi, K.; Murakami, S.
submitted to the EMBL Data Library, September 1991
A>Description: A whole genome of hepatitis C virus cDNA was isolated from a single patient
A:Reference number: S18028

A:Accession: S18030
A:Molecule type: genomic RNA
A:Residues: 1-3010 <HNP>
A:Cross-references: UNIPROT:P06849; EMBL:X61596; NID:G95478; PIDN:CAA43793.1; PID:G95479797
R:Experimental source: isolate JKI from an individual
R:Honda, M.; Keneko, S.; Unoura, M.; Kobayashi, K.; Murakami, S.
Arch. Virol. 128, 163-169, 1993
A>Title: Sequence analysis of putative structural regions of hepatitis C virus isolated
A:Reference number: A48332; MUID:93119270; PMID:8380322

A:Accession: S33570
A:Molecule type: genomic RNA
A:Residues: 1-547,'T','548-621','V','623-624','S','626-652','DL','655-761','T','763-782'<HOW>
A:CROSS-references: EMBL:X61591
A>Note: This sequence is inconsistent with the nucleotide translation
A>Note: The authors translated the codon AGG for residue 43 as Pro, TGG for residue 320
as Trp, and TTC for residue 771 as Ser
A>Note: Sequence extracted from NCBI backbone (NCBIN:121747, NCBIF:121748)
C:Superfamily: hepatitis C virus genome polyprotein
C:Keywords: ATp; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; serin
F:2-115/Product: capsid protein C #status predicted <CPC>
F:116-131/Product: envelope protein M #status predicted
F:139-389/Product: major envelope protein E #status predicted <MEES>
F:390-729/Product: nonstructural protein NS1 #status predicted <NS1>
F:730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
F:1007-1615/Product: hepativirin #status predicted <NS3>
F:1230-1237/Region: nucleotide-binding motif A (P-loop)
F:1312-1317/Region: nucleotide-binding motif B
F:1316-1319/Region: DEXH motif
F:1616-1862/Product: nonstructural protein NS4a #status predicted <NS4a>
F:1863-2013/Product: nonstructural protein NS4b #status predicted <NS4b>
F:2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F:1196, 209, 224, 250, 305, 417, 423, 448, 532, 540, 556, 576, 623, 645/Binding site: carbohydrate (AE

Query Match 84.7% ; Score 277; DB 1; Length 3010;
Best Local Similarity 84.1% ; Pred. No. 4,4e+23;
Matches 53; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Oy 1 ALLENLVINAASAACTGILMFLVFECAMVYKGLVFGATYSLLGWPLLLLLALAPOR 60
DB 747 ALLENVLVNAASVAGAHGISFLVFECAMVIKRLVPGAAVAFGVWPLLALLALPPR 806

Oy 61 AVA 63
DB |||
Db 807 AVA 809

RESULT 3
genome polyprotein - hepatitis C virus (strain J)

N:Contains: capsid protein C; envelope protein M; major envelope protein E; nonstructura
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C:Species: hepatitis C virus
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: AJ9253; PS0086
R:Ikato, N.; Hijioka, M.; Ootsuyama, Y.; Nakagawa, M.; Ohkoshi, S.; Sugimura, T.; Shimoto
Proc. Natl. Acad. Sci. U.S.A. 87, 9524-9528, 1990
A>Title: Molecular cloning of the human hepatitis C virus genome from Japanese patients
A:Reference number: AJ9253; MUID:91088550; PMID:2175903

A:Accession: AJ9253
A:Molecule type: genomic RNA
A:Residues: 1-3010 <KAT>
A:CROSS-references: UNIPROT:P26662; GB:D90208; NID:G221610; PIDN:BA414233.1; PID:G22161111
R:Ikato, N.; Ohkoshi, S.; Shimotohno, K.
Proc. Jpn. Acad. 65B, 219-223, 1989
A>Title: Japanese isolates of the non-A, non-B hepatitis viral genome show sequence vari
A:Accession: PS0086

A: Molecule type: genomic RNA
 A: Residues: 2650-2707 <RA2>
 A: Experimental source: Japanese isolate
 C: Comment: The cleavage sites of this polyprotein have not been determined.
 C: Superfamily: hepatitis C virus genome polyprotein
 C: Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; serin
 F:12-115/Product: capsid protein C #status predicted <PPC>
 F:116-191/Product: envelope protein M #status predicted <EPM>
 F:192-389/Product: major envelope protein E #status predicted <MEB>
 F:390-729/Product: nonstructural protein NS1 #status predicted <NS1>
 F:730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
 F:1007-1615/Product: hepatitisin #status predicted <NS3>
 F:1230-1237/Region: nucleotide-binding motif A (P-loop)
 F:1312-1317/Region: nucleotide-binding motif B
 F:1316-1319/Region: DEXH motif
 F:1616-1862/Product: nonstructural protein NS4 #status predicted <N4A>
 F:1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
 F:2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
 F:1196,209,234,305,325,417,423,430,446,532,540,556,576,623,645,1213,1255,2041,2077,2240,2

Query Match 84.1% Score 275; DB 1; Length 3010;
 Best Local Similarity 83.9% Pred. No. 7.3e-23;
 Matches 52; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 LEN:VYVNAASAGCTHILMFVFPFCAAWYKGRLVGARYSLGLMPLLLLLALPORA 61
 DB 748 LEN:VYVNAASVAGAHGLSLFVFPFCAAWYIKRLLVPGAAVYALYGVPLLLLLLALPPRA 807
 QY 62 YA 63
 DB 808 YA 809

RESULT 4
 GNMVCH
 genome polyprotein - hepatitis C virus (strain H)
 M: Contains: capsid protein C; envelope protein M; hepatitisin (HC 3.4.21.98) (nonstructu
 protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
 C: Species: hepatitis C virus
 A: Note: host Homo sapiens (man)
 C: Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
 C: Accession: A36814; A41546
 R: Rinnhauppe, G.; Zebdeed, S.; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.M.
 submitted to GenBank, July 1992
 A: Description: Genomic structure of the human prototype strain H of hepatitis C virus: c
 A: Reference number: A36814
 A: Accession: A36814
 A: Molecule type: genomic RNA
 A: Residues: 1-3011 <NMC>
 A: Cross-references: UNIPROT:P27956; GB:M67463; NID:g329737; PID:AAA45534.1; PID:g329738
 R: Rinnhauppe, G.; Zebdeed, S.; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.M.
 Proc. Natl. Acad. Sci. U.S.A. 88, 10292-10296, 1991
 A: Title: Genomic structure of the human prototype strain H of hepatitis C virus: compari
 A: Reference number: A41546; MUID:92052256; PMID:1658800
 A: Contents: annotation
 A: Note: neither amino acid nor nucleotide sequence is given
 C: Superfamily: hepatitis C virus genome polyprotein
 C: Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructura
 C: F:11-115/Product: capsid protein C #status predicted <PPC>
 F:116-191/Product: envelope protein M #status predicted <EPM>
 F:192-389/Product: major envelope protein E #status predicted <MEB>
 F:390-729/Product: nonstructural protein NS1 #status predicted <NS1>
 F:730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
 F:1007-1615/Product: hepatitisin #status predicted <NS3>
 F:1230-1237/Region: nucleotide-binding motif A (P-loop)
 F:1312-1317/Region: nucleotide-binding motif B
 F:1316-1319/Region: DEXH motif
 F:1616-1862/Product: nonstructural protein NS4 #status predicted <N4A>
 F:1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
 F:2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
 F:1196,209,234,305,325,417,423,430,446,532,540,556,576,623,645,1213,1255,2041,2240,23

Query Match 83.2% Score 272; DB 1; Length 3011;

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Best Local Similarity 81.0%; Pred. No. 1.6e-22;
Matches 51; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Oy 1 ALENLVNNAASAGTGHILMFLVFCAMVYKGRIVPGATYSLLGLMPLLLLLALPQR 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 747 ALENLVNNAASLAGTGLVSVFLVFCAMVYKGRVGAVALYGMPLLLLLALPQR 806
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Oy 61 AYA 63
    |||
Db 807 AYA 809

RESULT 5
A45573
genome polyprotein - hepatitis C virus (strain J7)
N:Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C:Species: hepatitis C virus
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: A45573
R:Tanaka, T.; Kato, N.; Nakagawa, M.; Ootsubayama, Y.; Cho, M.J.; Nakazawa, T.; Hijikata,
virus Res. 23, 39-53, 1992
A:Title: Molecular cloning of hepatitis C virus genome from a single Japanese carrier: B
A:Reference number: A45573; MUID:92295714; PMID:1318627
A:Accession: A45573
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-3010 <TM>
A:Cross-references: UNIPROT:000269; GB:D11168; GB:D01171; NID:G221612; PIDN:BA01943.1;
A:Experimental source: HCV-JT
A>Note: Sequence extracted from NCBI backbone (NCBIN:106206, NCBI:P.106207)
C:Superfamily: hepatitis C virus genome polyprotein
C:Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; serin
F:12-115/Product: capsid protein C #status predicted <CPC>
F:116-191/Product: envelope protein M #status predicted <EPM>
F:192-389/Product: major envelope protein E #status predicted <ME>
F:390-729/Product: nonstructural protein NS1 #status predicted <NS1>
F:730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
F:1007-1615/Product: hepacivirin #status predicted <NS3>
F:1230-1237/Region: nucleotide-binding motif A (P-loop)
F:1312-1319/Region: DEXH motif
F:1316-1319/Region: DEXH motif
F:1616-1862/Product: nonstructural protein NS4a #status predicted <NS4a>
F:1663-2013/Product: nonstructural protein NS4b #status predicted <NS4b>
F:196-209,233,234,250,305,325,417,423,430,448,532,540,556,576,623,645,1213,1255,2041,207
F:196-209,233,234,250,305,325,417,423,430,448,532,540,556,576,623,645,1213,1255,2041,207

Query Match 82.9%; Score 271; DB 1; Length 3010;
Best Local Similarity 84.1%; Pred. No. 2.1e-22;
Matches 53; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Oy 1 ALENLVNNAASAGTGHILMFLVFCAMVYKGRIVPGATYSLLGLMPLLLLLALPQR 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 747 ALENLVNNAASLAGADILSVLFVFCAMVYKGRVGAVALYGMPLLLLLALPQR 806
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Oy 61 AYA 63
    |||
Db 807 AYA 809

RESULT 6
GNMVTM
genome polyprotein - hepatitis C virus (strain Taiwan)
N:Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C:Species: hepatitis C virus
A>Note: host Homo sapiens (man)
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C:Accession: A40244
R:Chen, P.J.; Lin, M.H.; Tai, K.F.; Liu, P.C.; Lin, C.J.; Chen, D.S.
virology 180, 102-113, 1992
A:Title: The Taiwanese hepatitis C virus genome: sequence determination and mapping the
A:Reference number: A40244; MUID:92230206; PMID:1314449
A:Accession: A40244

```

```

A:Molecule type: genomic RNA
A:Residues: 1-3010 <CH>
A:Cross-references: UNIPROT:P29846; GB:M84754
A:Superfamily: hepatitis C virus genome polyprotein
C:Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructura
F:1-115/Product: capsid protein C #status predicted <CPC>
F:116-191/Product: envelope protein M #status predicted <EPM>
F:192-389/Product: major envelope protein E #status predicted <ME>
F:390-729/Product: nonstructural protein NS1 #status predicted <NS1>
F:730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
F:1007-1615/Product: hepacivirin #status predicted <NS3>
F:1230-1237/Region: nucleotide-binding motif A (P-loop)
F:1312-1319/Region: DEXH motif
F:1316-1319/Region: DEXH motif
F:1616-1862/Product: nonstructural protein NS4a #status predicted <NS4a>
F:1663-2013/Product: nonstructural protein NS4b #status predicted <NS4b>
F:196-209,233,234,250,305,325,417,423,430,448,532,540,556,576,623,645,1213,1255,2041,207
F:196-209,233,234,250,305,325,417,423,430,448,532,540,556,576,623,645,1213,1255,2041,207

Query Match 82.9%; Score 271; DB 1; Length 3010;
Best Local Similarity 82.5%; Pred. No. 2.1e-22;
Matches 52; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Oy 1 ALENLVNNAASAGTGHILMFLVFCAMVYKGRIVPGATYSLLGLMPLLLLLALPQR 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 747 ALENLVNNAASVAGMGHTLSFLVFCAMVYKGRVGAVALYGMPLLLLLALPQR 806
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Oy 61 AYA 63
    |||
Db 807 AYA 809

RESULT 7
GNMVT3
genome polyprotein - hepatitis C virus (strain HCV-1)
N:Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C:Species: hepatitis C virus
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: A39166; PQ0403; PQ0404
R:Choo, Q.L.; Richman, K.H.; Han, J.H.; Berger, K.; Lee, C.; Dong, C.; Gallegos, C.; Coi
Proc. Natl. Acad. Sci. U.S.A. 88, 2451-2455, 1991
A:Title: Genetic organization and diversity of the hepatitis C virus.
A:Reference number: A39166; MUID:91172826; PMID:1848704
A:Accession: A39166
A:Molecule type: mRNA
A:Residues: 1-3011 <CHO>
A:Cross-references: UNIPROT:P26664; GB:M62321; NID:G329873; PIDN:AAA45676.1; PID:G329874
R:Chan, S.W.; McMahon, F.; Holmes, E.C.; Dow, B.; Peutherer, J.F.; Follett, E.; Yap, P.L
J. Gen. Virol. 73, 1131-1141, 1992
A:Title: Analysis of a new hepatitis C virus type and its phylogenetic relationship to e
A:Reference number: PQ0393; MUID:92268871; PMID:1316939
A:Accession: PQ0403
A:Molecule type: genomic RNA
A:Residues: 1577-1633 <CHA>
A:Cross-references: DDBJ:D10128
A:Experimental source: isolates E-B16
A:Accession: PQ0404
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1577-1633 <CH2>
A:Experimental source: isolates E-B17
A:Superfamily: hepatitis C virus genome polyprotein
C:Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructura
F:1-115/Product: capsid protein C #status predicted <CPC>
F:116-191/Product: envelope protein M #status predicted <EPM>
F:192-389/Product: major envelope protein E #status predicted <ME>
F:390-729/Product: nonstructural protein NS1 #status predicted <NS1>
F:730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
F:1007-1615/Product: hepacivirin #status predicted <NS3>
F:1230-1237/Region: nucleotide-binding motif A (P-loop)
F:1312-1319/Region: nucleotide-binding motif B
F:1316-1319/Region: DEXH motif

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F:1616-1862/Product: nonstructural protein NS4a #status predicted <NA>
F:1861-2013/Product: nonstructural protein NS4b #status predicted <NA>
F:2014-3011/Product: nonstructural protein NS5 #status predicted <NS>
F:196,209,234,305,325,417,423,430,448,476,532,540,556,576,623,645,1213,1255,2041,2077,22

Query Match 81.0%; Score 265; DB 1; Length 3011;
Best Local Similarity 77.8%; Pred. No. 9, 9e-22;

Matches 49; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ALENVLVLAASAGTGHILMFLVFCAMVYKGRVLPATYSLLGLMPLLLLLALPQR 60

DB 747 ALENVLVLAASAGTGHILMFLVFCAMVYKGRVLPATYSLLGLMPLLLLLALPQR 806

QY 61 AYA 63

DB 807 AYA 809

RESULT 8

S40770 genome polyprotein - hepatitis C virus

N:Contains: capsid protein C; envelope protein M; hepatitis C virus (EC 3.4.21.98) (nonstructu

C:Species: hepatitis C virus

C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004

C:Accession: S40770; FCI285

R:Okamoto, H.

submitted to the EMBL Data Library, March 1992

A:Reference number: S40770

A:Accession: S40770

A:Molecule type: genomic RNA

A:Residues: 1-3011 <OK>

A:Cross-references: UNIPROT:Q03463; EMBL:DI0749; NID:G221586; PIDN:BA01582.1; PID:G2215

R:Okamoto, H.; Okada, S.; Sugiyama, Y.; Yotsunoto, S.; Tanaka, T.; Yoshizawa, H.; Tsuda,

Jpn. J. Exp. Med. 60, 167-177, 1990

A:Title: The 5'-terminal sequence of the hepatitis C virus genome.

A:Reference number: FCI284; MUID:91013116; PMID:2170712

A:Accession: FCI285

A:Molecule type: genomic RNA

A:Residues: 1-513 <OK>

A:Cross-references: GB:D00831; NID:G221511; PIDN:BA00705.1; PID:G221512

A:Experimental source: isolate HC-J1

C:Superfamily: hepatitis C virus genome polyprotein

C:Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; serin

F:2-115/Product: capsid protein C #status predicted <CPC>

F:116-191/Product: envelope protein M #status predicted <EPW>

F:192-389/Product: major envelope protein E #status predicted <MEB>

F:390-729/Product: nonstructural protein NS1 #status predicted <NS1>

F:730-1006/Product: nonstructural protein NS2 #status predicted <NS2>

F:1007-1615/Product: hepatitis C virus genome polyprotein

F:1230-1237/Region: nucleotide-binding motif A (P-loop)

F:1312-1317/Region: nucleotide-binding motif B

F:1316-1319/Region: DEXH motif

F:1616-1862/Product: nonstructural protein NS4a #status predicted <NA>

F:1861-2013/Product: nonstructural protein NS4b #status predicted <NA>

F:2014-3011/Product: nonstructural protein NS5 #status predicted <NS>

Query Match 80.7%; Score 264; DB 1; Length 3011;
Best Local Similarity 79.4%; Pred. No. 1, 3e-21;

Matches 50; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ALENVLVLAASAGTGHILMFLVFCAMVYKGRVLPATYSLLGLMPLLLLLALPQR 60

DB 747 ALENVLVLAASAGTGHILMFLVFCAMVYKGRVLPATYSLLGLMPLLLLLALPQR 806

QY 61 AYA 63

DB 807 AYA 809

RESULT 9

GNMVJ8 genome polyprotein - hepatitis C virus (strain HC-J8)

N:Contains: capsid protein C; envelope protein M; hepatitis C virus (EC 3.4.21.98) (nonstructu

C:Species: hepatitis C virus

C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004

C:Accession: A40250; PQ0397; PQ0559

R:Okamoto, H.; Kurai, K.; Okada, S.; Yamamoto, K.; Iizuka, H.; Tanaka, T.; Fukuda, S.;

Virology 188, 331-341, 1992

A:Title: Full-length sequence of a hepatitis C virus genome having poor homology to repo

A:Reference number: A40250; MUID:92230232; PMID:1314459

A:Accession: A40250

A:Molecule type: genomic RNA

A:Residues: 1-1033 <OK>

A:Cross-references: UNIPROT:P26661; GB:D10988; GB:D01221; NID:G221608; PIDN:BA01761.1;

R:Chan, S.W.; McMahon, F.; Holmes, E.C.; Dow, B.; Peutherer, J.F.; Follett, E.; Yap, P.L

J. Gen. Virol. 73, 1131-1141, 1992

A:Title: Analysis of a new hepatitis C virus type and its phylogenetic relationship to e

A:Reference number: PQ0393; MUID:92268871; PMID:1316939

A:Accession: PQ0397

A:Molecule type: genomic RNA

A:Residues: 2678-2754 <CHA>

A:Cross-references: DDBJ:DI0134

A:Experimental source: isolate E-b12

R:Kato, N.; Ootsuyama, Y.; Ohkoshi, S.; Nakazawa, T.; Mori, S.; Hijikata, M.; Shimotohno

Biochem. Biophys. Res. Commun. 181, 279-285, 1991

A:Title: Distribution of plural HCV types in Japan.

A:Reference number: PQ0554; MUID:92068204; PMID:1720309

A:Accession: PQ0559

A:Molecule type: mRNA

A:Residues: 2678-2729 <KAT>

A:Cross-references: GB:D10567; GB:D90518; NID:G221523; PIDN:BA01418.1; PID:G221524

C:Superfamily: hepatitis C virus genome polyprotein

C:Keywords: ATP; capsid protein C; envelope protein; glycoprotein; hydrolase; nonstructura

F:1-115/Product: capsid protein C #status predicted <CPC>

F:116-191/Product: envelope protein M #status predicted <EPW>

F:192-389/Product: major envelope protein E #status predicted <MEB>

F:390-733/Product: nonstructural protein NS1 #status predicted <NS1>

F:734-1010/Product: nonstructural protein NS2 #status predicted <NS2>

F:1011-1619/Product: hepatitis C virus genome polyprotein

F:1234-1241/Region: nucleotide-binding motif A (P-loop)

F:1316-1321/Region: nucleotide-binding motif B

F:1320-1323/Region: DEXH motif

F:1620-1866/Product: nonstructural protein NS4a #status predicted <NA>

F:1867-2017/Product: nonstructural protein NS4b #status predicted <NA>

F:2018-3033/Product: nonstructural protein NS5 #status predicted <NS>

F:196,209,233,299,305,417,423,430,448,477,534,542,558,578,627,649,1091,1217,1259,2038,23

Query Match 71.6%; Score 234; DB 1; Length 3033;
Best Local Similarity 68.3%; Pred. No. 3, 2e-18;

Matches 43; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALENVLVLAASAGTGHILMFLVFCAMVYKGRVLPATYSLLGLMPLLLLLALPQR 60

DB 751 ALEKLIHSASASANGPLWFIFPTAWYLKGRVVPATYSVLGLMPLLLVLPQQ 810

QY 61 AYA 63

DB 811 AYA 813

RESULT 10

J01303 genome polyprotein - hepatitis C virus (isolate HC-J6)

N:Contains: capsid protein C; envelope protein M; hepatitis C virus (EC 3.4.21.98) (nonstructu

C:Species: hepatitis C virus

C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004

C:Accession: J01303

R:Okamoto, H.; Okada, S.; Sugiyama, Y.; Kurai, K.; Iizuka, H.; Machida, A.; Miyakawa, Y.

J. Gen. Virol. 72, 2697-2704, 1991

A:Title: Nucleotide sequence of the genomic RNA of hepatitis C virus isolated from a hum

A:Reference number: J01303; MUID:92044440; PMID:1658196

A:Accession: J01303

A:Molecule type: genomic RNA

A:Residues: 1-3033 <OKA>
A:Cross-references: UNIPROT:P26660; GB:D00944; NID:G221650; PIDN:BA00792.1; PID:G221651
A:Experimental source: isolate HC-J6 from a Japanese individual
C:Superfamily: hepatitis C virus genome polypeptide
C:Keywords: ATP; glycoprotein; hydroxylase; P-loop; polypeptide; serine proteinase; transmembrane
F:12-115/Product: capsid protein C #status predicted <CPC>
F:116-191/Product: envelope protein M #status predicted <EPM>
F:193-389/Product: major envelope protein E #status predicted <MEB>
F:390-733/Product: nonstructural protein NS1 #status predicted <NS1>
F:734-1010/Product: nonstructural protein NS2 #status predicted <NS2>
F:1011-1619/Product: hepativirin #status predicted <NS3>
F:11316-13321/Region: nucleotide-binding motif B
F:11320-13323/Region: DEXH motif
F:1620-1866/Product: nonstructural protein NS4b #status predicted <NS4b>
F:1867-2017/Product: nonstructural protein NS5 #status predicted <NS5>
F:2018-3033/Product: nonstructural protein NS5 #status predicted <NS5>
F:196,209,224,305,325,417,423,430,448,477,534,542,558,578,627,649,1091,1217,1259,2038,28

Query Match 69.4%; Score 227; DB 1; Length 3033;
Best Local Similarity 71.4%; Pred. No. 2e-17;
Matches 45; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Oy 1 ALENLVNNAASAGTHGILMFVFCAMVYKGRVPGATYSLLGLMPLLLLLALPQR 60
Db 751 ALEKLVNNAASASCSNGFLVFVIFVAVAMVYKGRVPLATYSLLGLMPLLLALPQQ 810

Oy 61 AYA 63
Db 811 AYA 813

RESULT 11
JCS620
genome polypeptide - hepatitis C virus (isolate ETH1480)
N:Contains: capsid protein C; envelope protein M; hepativirin (EC 3.4.21.98) (nonstructural protein NS4b; nonstructural protein NS5)
C:Species: hepatitis C virus
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: JCS620
R:Chamberlain, R.W.; Adams, N.J.; Taylor, L.A.; Simmonds, P.; Elliott, R.M.
Biochem. Biophys. Res. Commun. 236, 44-49, 1997
A:Title: The complete coding sequence of hepatitis C virus genotype 5a, the predominant A:Reference number: JCS620; MUID:9736593; PMID:9223423
A:Accession: JCS620
A:Molecule type: mRNA
A:Residues: 1-3014 <CHN>
A:Cross-references: UNIPROT:O39928; GB:Y13184
A:Experimental source: genotype 5a, which predominates in South Africa
A>Note: the translation of the nucleotide sequence is not complete in this paper
C:Superfamily: hepatitis C virus genome polypeptide
C:Keywords: ATP; glycoprotein; hydroxylase; nucleotide binding; P-loop; polypeptide; serine
F:12-115/Product: capsid protein C #status predicted <CPC>
F:116-191/Product: envelope protein M #status predicted <EPM>
F:193-389/Product: major envelope protein E #status predicted <MEB>
F:390-733/Product: nonstructural protein NS1 #status predicted <NS1>
F:734-1010/Product: nonstructural protein NS2 #status predicted <NS2>
F:1008-1616/Product: hepativirin #status predicted <NS3>
F:11313-1318/Region: nucleotide-binding motif A (P-loop)
F:11317-1320/Region: nucleotide-binding motif B
F:1617-1863/Product: nonstructural protein NS4b #status predicted <NS4b>
F:1864-2014/Product: nonstructural protein NS5 #status predicted <NS5>
F:2015-3014/Product: nonstructural protein NS5 #status predicted <NS5>
F:2210-2249/Region: interferon sensitivity determining #status predicted

Query Match 64.8%; Score 212; DB 1; Length 3014;
Best Local Similarity 63.9%; Pred. No. 9.9e-16;
Matches 39; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

Oy 3 ALENLVNNAASAGTHGILMFVFCAMVYKGRVPGATYSLLGLMPLLLLLALPQR 62
Db 750 ALEKLVNNAASASCSNGFLVFVIFVAVAMVYKGRVPLATYSLLGLMPLLLALPQQ 809

Oy 63 A 63
Db 810 A 810

RESULT 12
S19876
genome polypeptide - hepatitis C virus (isolate JK5) (fragment)
N:Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein
C:Species: hepatitis C virus
A:Variety: isolate JK5
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: S19876
R:Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
submitted to the EMBL Data Library, September 1991
A:Description: Sequence analysis of putative structural regions of Hepatitis C Virus iso
A:Reference number: S18029
A:Accession: S19876
A:Molecule type: genomic RNA
A:Residues: 1-782 <HON>
A:Cross-references: UNIPROT:Q68953; EMBL:X61595; NID:G59486; PIDN:CAA43792.1; PID:G59487
A:Experimental source: isolate JK5
C:Superfamily: hepatitis C virus genome polypeptide
C:Keywords: capsid protein; core protein; envelope protein; glycoprotein; nonstructural
F:1-191/Product: core protein #status predicted <MAT1>
F:193-383/Product: envelope protein 1 #status predicted <MAT2>
F:384-733/Product: NS1/E2 protein #status predicted <MAT3>
F:734-782/Product: nonstructural protein 2 (fragment) #status predicted <MAT4>

Query Match 50.8%; Score 166; DB 2; Length 782;
Best Local Similarity 88.9%; Pred. No. 4.6e-11;
Matches 32; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 ALENLVNNAASAGTHGILMFVFCAMVYKGR 36
Db 747 ALENLVNNAASVAGAHGILMFVFCAMVYKGR 782

RESULT 13
S18032
genome polypeptide - hepatitis C virus (isolate JK4) (fragment)
N:Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein
C:Species: hepatitis C virus
A:Variety: isolate JK4
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: S18032
R:Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
submitted to the EMBL Data Library, September 1991
A:Description: Sequence analysis of putative structural regions of Hepatitis C Virus iso
A:Reference number: S18029
A:Accession: S18032
A:Molecule type: genomic RNA
A:Residues: 1-782 <HON>
A:Cross-references: UNIPROT:Q68952; EMBL:X61594
A:Experimental source: isolate JK4
C:Superfamily: hepatitis C virus genome polypeptide
C:Keywords: capsid protein; core protein; envelope protein; glycoprotein; nonstructural
F:1-191/Product: core protein #status predicted <MAT1>
F:193-383/Product: envelope protein 1 #status predicted <MAT2>
F:384-733/Product: NS1/E2 protein #status predicted <MAT3>
F:734-782/Product: nonstructural protein 2 (fragment) #status predicted <MAT4>

Query Match 50.2%; Score 164; DB 2; Length 782;
Best Local Similarity 86.1%; Pred. No. 7.7e-11;
Matches 31; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 1 ALENLVNNAASAGTHGILMFVFCAMVYKGR 36
Db 747 ALENLVNNAASVAGAHGILMFVFCAMVYKGR 782

RESULT 14

P00677
 hypochlorite protein 787 - hepatitis C virus (fragment)
 C:Species: hepatitis C virus
 C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
 C:Accession: P00677
 R:Cho, S.H.; Yoon, J.I.; Chang, J.E.; Ahn, B.M.; Lee, C.H.; Lee, Y.I.
 Biochem. Biophys. Res. Commun. 196, 780-788, 1993
 A:Title: Genomic typing of hepatitis C viruses from Korean patients: Implications of gen
 A:Reference number: P00677; MUID:94059104; PMID:8240354
 A:Accession: P00677
 A:Molecule type: mRNA
 A:Residues: 1-787 <CHO>
 A:Cross-references: UNIPROT:Q08244; GB:L20498; NID:g1381031; PIDN:AA02608.1; PID:g13810
 C:Superfamily: hepatitis C virus genome polypeptide
 C:Keywords: glycoprotein; nonstructural protein
 F:196, 209, 234, 250, 305, 325, 421, 427, 452, 536, 544, 560, 580, 627, 649/Binding site: carbohydrate

Query Match	49.2%	Score 161;	DB 2;	Length 787;
Best Local Similarity	83.8%;	Pred. No. 1.7e-10;		
Matches 31;	Conservative 2;	Mismatches 4;	Indels 0;	Gaps 0;

```

QY      1 ALENLVLTNAAAGATHGILMTLVFPCAAWYVKGRIV 37
        ||||| | | | | | | | | | | | | | | | |
DB      751 ALENLVLTNAAAYVAGAHGILSELVFPCAAWYIKGLIV 787

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RESULT 15

genome polyprotein - hepatitis C virus (isolate JK) (fragment)
 N:Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein
 C:Species: hepatitis C virus
 A:Variety: isolate JK
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C:Accession: S19875
 R:Horita, M.; Kaneo, S.; Maeshi, U.; Kobayashi, K.; Murakami, S.
 submitted to the EMBL Data Library, September 1991
 A:Description: Sequence analysis of putative structural regions of Hepatitis C Virus iso
 A:Reference number: S18029
 A:Accession: S19875
 A:Molecule type: genomic RNA
 A:Residues: 1-782 <HON>
 A:Cross-references: UNIPROT:068951; EMBL:X61592; NID:G959482; PIDN:CAA43789.1; PID:G959483
 A:Experimental source: isolate JK
 A:Superfamily: hepatitis C virus genome polyprotein
 C:Keywords: capsid protein; core protein; envelope protein; glycoprotein; nonstructural
 F:1-191/Product: core protein #status predicted <MAT1>
 F:192-383/Product: envelope protein 1 #status predicted <MAT2>
 F:384-733/Product: NS1/E2 protein #status predicted <MAT3>
 F:734-782/Product: nonstructural protein 2 (fragment) #status predicted <MAT4>

Query Match	48.9%	Score 160;	DB 2;	Length 762;
Best Local Similarity	86.1%;	Pred. No. 2.2e-10;		
Matches	31; Conservative	2; Mismatches	3; Indels	0; Gaps 0;

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Qy      1 ALENVLVNAASACTHGIMFLVFPCAAIVYKGL 36
          |||||  : |||||  : |||||
Db      747 ALENVLVNAASVAGTRGIPFLVFPCAAIYIKGL 783

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Search completed: October 4, 2005, 18:57:53
Job time : 16 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2005, 18:41:15 ; Search time 63 Seconds
(without alignments)
512.079 Million cell updates/sec

Title: US-10-669-175-1
Perfect score: 327
Sequence: 1 ALENLVVNAASAACTHGIL.....LLGLWPLLLLLLPORAVA 63

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_crembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	286	87.5	3010	2	Q9J3H7 hepatitis c
2	285	87.2	3010	2	Q68533 hepatitis c
3	284	86.9	3010	2	Q9J3G8 hepatitis c
4	283	86.9	3010	2	Q9J3H1 hepatitis c
5	283	86.5	3010	1	POLG_HCVBK P26663 h genome po
6	282	86.2	3010	2	Q8V638 hepatitis c
7	282	86.2	3010	2	Q9J3F9 hepatitis c
8	282	86.2	3010	2	Q9Q1X3 hepatitis c
9	281	85.9	562	2	Q98UN3 hepatitis c
10	281	85.9	1117	2	Q80P91 hepatitis c
11	281	85.9	3010	2	Q68826 hepatitis c
12	281	85.9	3010	2	Q6GYR9 hepatitis c
13	281	85.9	3010	2	Q9DTE1 hepatitis c
14	281	85.9	3010	2	Q9J3G3 hepatitis c
15	281	85.9	3010	2	Q9J3G6 hepatitis c
16	281	85.9	3010	2	Q9Q1X4 hepatitis c
17	281	85.9	3010	2	Q9Q1X5 hepatitis c
18	281	85.9	3010	2	Q9Q1X5 hepatitis c
19	281	85.9	3010	2	Q9Q1X5 hepatitis c
20	281	85.9	3010	2	Q9Q1X5 hepatitis c
21	280	85.6	3010	2	Q81541 hepatitis c
22	280	85.6	3010	2	Q81541 hepatitis c
23	280	85.6	3010	2	Q9J3G0 hepatitis c
24	280	85.6	3010	2	Q9J3G1 hepatitis c
25	280	85.6	3010	2	Q9J3H4 hepatitis c
26	279	85.3	3010	2	Q68285 hepatitis c
27	279	85.3	3010	2	Q68285 hepatitis c
28	279	85.3	3010	2	Q68285 hepatitis c
29	279	85.3	3010	2	Q68285 hepatitis c
30	278	85.0	3010	2	Q9J3G2 hepatitis c
31	278	85.0	3010	2	Q9J3G2 hepatitis c

32	278	85.0	3010	2	Q9J3G5 hepatitis c
33	278	85.0	3013	2	Q9Q1X9 hepatitis c
34	278	85.0	3013	2	Q9Q1Y0 hepatitis c
35	277	84.7	3010	2	P90192 hepatitis c
36	277	84.7	3010	2	P90195 hepatitis c
37	277	84.7	3010	2	Q68949 hepatitis c
38	277	84.7	3010	2	Q81760 hepatitis c
39	277	84.7	3010	2	Q9J3I0 hepatitis c
40	277	84.7	3010	2	Q9Q1X6 hepatitis c
41	277	84.7	3010	2	Q9Q1X7 hepatitis c
42	277	84.7	3010	2	Q9Q1X8 hepatitis c
43	277	84.7	3010	2	Q9Q1Y5 hepatitis c
44	277	84.7	3010	2	Q9Q1Y6 hepatitis c
45	277	84.7	3010	2	Q9Q1X8 hepatitis c

ALIGNMENTS

RESULT 1
ID Q9J3H7 PRELIMINARY; PRT; 3010 AA.
AC Q9J3H7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Polypeptide.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RC SEQUENCE FROM N.A.
RA Nagayama K., Kurosaki M., Enomoto N., Miyaoka Y., Marumo F., Sato C.;
RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF207756; AAF65946.1; -
DR PIR; A61196; A61196.
DR PIR; P00246; P00246.
DR PIR; P00804; P00804.
DR PIR; PS0329; PS0329.
DR HSP; Q8Y31; ICWX.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019021; C:Viral envelope; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0008236; F:serine-type peptidase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR GO; GO:0019087; P:viral transformation; IEA.
DR InterPro; IPR000345; Cyrc_heme_BS.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR002522; HCV capsid.
DR InterPro; IPR002521; HCV core.
DR InterPro; IPR002519; HCV env.
DR InterPro; IPR002531; HCV NS1.
DR InterPro; IPR000745; HCV NS4A.
DR InterPro; IPR001490; HCV NS4B.
DR InterPro; IPR002868; HCV NS5A.
DR InterPro; IPR002166; HCV RdRp.
DR InterPro; IPR004109; Peptidase_S29.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR002518; Pept_U39_HCV_NS2.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR Pfam; PF01542; HCV_core; 1.
DR Pfam; PF01542; HCV_core; 1.

DR Pfam; PF01539; HCV_env; 1.
 DR Pfam; PF01560; HCV_NS1; 1.
 DR Pfam; PF01538; HCV_NS2; 1.
 DR Pfam; PF02307; HCV_NS3; 1.
 DR Pfam; PF01006; HCV_NS4a; 1.
 DR Pfam; PF01001; HCV_NS4b; 1.
 DR Pfam; PF01506; HCV_NS5a; 1.
 DR Pfam; PF00998; Viral_RdRp; 1.
 DR SMART; SM00487; DEXDC; 1.
 DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
 DR Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
 KM Polyprotein; Transmembrane.
 SQ SEQUENCE 3010 AA; 327366 MW; D863F7317FFA106 CRC64;

Query Match 87.5%; Score 286; DB 2; Length 3010;
 Best Local Similarity 87.3%; Pred. No. 1.7e-23;
 Matches 55; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 ALENLVNNAASAGTHGILWLFPCAAWYKGRLVPGATYSLLGLPFLILLALPQR 60
 DB 747 ALENLVNNAASVAGTHGILSFVFPCCAAWYKGRLVPGAAVALYGVWPLILLALPQR 806

QY 61 AYA 63
 DB 807 AYA 809

RESULT 2
 068533 PRELIMINARY; PRT; 3010 AA.

AC 068533;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Polyprotein.
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxId=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mueller H.M., Pfaff E., Heller A.E., Goeseer T., Theilmann L.;
 RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
 DR EMBL; U5476; AAA66907.1; -
 DR PIR; A61196; A61196.
 DR HSP; 08YJ51; ICWX.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0006026; F:ATP-dependent helicase activity; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
 DR GO; GO:0008236; F:serine-type peptidase activity; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR GO; GO:0019079; P:viral genome replication; IEA.
 DR GO; GO:0019087; P:viral transformation; IEA.
 DR InterPro; IPR000345; CytC_heme_BS.
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR011545; DEAD/DEAH N.
 DR InterPro; IPR011492; Flavi_DEAD.
 DR InterPro; IPR002522; HCV_capsid.
 DR InterPro; IPR002521; HCV_core.
 DR InterPro; IPR002519; HCV_env.
 DR InterPro; IPR002531; HCV_NS1.
 DR InterPro; IPR00745; HCV_NS4a.
 DR InterPro; IPR001490; HCV_NS4b.
 DR InterPro; IPR002868; HCV_NS5a.
 DR InterPro; IPR002166; HCV_RdRp.
 DR InterPro; IPR001650; Helicase_C.
 DR InterPro; IPR004109; Peptidase_S29.

DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR002518; Pept_U39_HCV_NS2.
 DR InterPro; IPR007095; RNA_pol_DS_PS.
 DR InterPro; IPR007094; RNA_pol_PSVlt.
 DR Pfam; PF07652; Flavi_DEAD; 1.
 DR Pfam; PF01543; HCV_capsid; 1.
 DR Pfam; PF01542; HCV_core; 1.
 DR Pfam; PF01539; HCV_env; 1.
 DR Pfam; PF01560; HCV_NS1; 1.
 DR Pfam; PF01538; HCV_NS2; 1.
 DR Pfam; PF02907; HCV_NS3; 1.
 DR Pfam; PF01006; HCV_NS4a; 1.
 DR Pfam; PF01001; HCV_NS4b; 1.
 DR Pfam; PF01506; HCV_NS5a; 1.
 DR Pfam; PF00271; Helicase_C; 1.
 DR Pfam; PF00998; Viral_RdRp; 1.
 DR SMART; SM00487; DEXDC; 1.
 DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
 DR Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
 KM Polyprotein; Transmembrane.
 SQ SEQUENCE 3010 AA; 327117 MW; 1D0B5A97C1466ED6 CRC64;

Query Match 87.2%; Score 285; DB 2; Length 3010;
 Best Local Similarity 87.3%; Pred. No. 2.2e-23;
 Matches 55; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 ALENLVNNAASAGTHGILWLFPCAAWYKGRLVPGATYSLLGLPFLILLALPQR 60
 DB 747 ALENLVNNAASLNGTHGILSFVFPCCAAWYKGRLVPGAAVALYGVWPLILLALPQR 806

QY 61 AYA 63
 DB 807 AYA 809

RESULT 3

AC 090368 PRELIMINARY; PRT; 3010 AA.

AD 090368;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Polyprotein.
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxId=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-EMD24;
 RA Nagayama K., Kurosaki M., Enomoto N., Miyasaka Y., Marumo F., Sato C.;
 RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF207765; AAF65955.1; -
 DR PIR; A61196; A61196.
 DR PIR; PS0328; PS0329.
 DR HSP; 08YJ51; ICWX.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
 DR GO; GO:0008236; F:serine-type peptidase activity; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR GO; GO:0019079; P:viral genome replication; IEA.
 DR GO; GO:0019087; P:viral transformation; IEA.
 DR InterPro; IPR000345; CytC_heme_BS.
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR011545; DEAD/DEAH N.
 DR InterPro; IPR002522; HCV_capsid.

DR InterPro; IPR002521; HCV_core.
 DR InterPro; IPR002519; HCV_env.
 DR InterPro; IPR002531; HCV_NS1.
 DR InterPro; IPR000745; HCV_NS4a.
 DR InterPro; IPR001490; HCV_NS4b.
 DR InterPro; IPR002868; HCV_NS5a.
 DR InterPro; IPR002166; HCV_RdRp.
 DR InterPro; IPR001650; Helicase_C.
 DR InterPro; IPR004109; Peptidase_S29.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR002518; Pept_U39_HCV_NS2.
 DR InterPro; IPR007095; RNA_pol_DS_PS.
 DR InterPro; IPR007094; RNA_pol_PSVir.
 DR Pfam; PF01543; HCV_capsid; 1.
 DR Pfam; PF01542; HCV_core; 1.
 DR Pfam; PF01539; HCV_env; 1.
 DR Pfam; PF01560; HCV_NS1; 1.
 DR Pfam; PF01538; HCV_NS2; 1.
 DR Pfam; PF02907; HCV_NS3; 1.
 DR Pfam; PF01006; HCV_NS4a; 1.
 DR Pfam; PF01001; HCV_NS4b; 1.
 DR Pfam; PF01506; HCV_NS5a; 1.
 DR Pfam; PF00271; Helicase_C; 1.
 DR Pfam; PF00998; Viral_RdRp; 1.
 DR SMART; SM00487; DEXDC; 1.
 DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
 DR Cost protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; Transmembrane.
 KM SEQUENCE 3010 AA; 326863 MW; E0BBB3528215457C CRC64;
 SQ

Query Match 86.9%; Score 284; DB 2; Length 3010;
 Best Local Similarity 85.7%; Pred. No. 2.9e-23;
 Matches 54; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 QY 1 ALENLVVNLNAAASAGTGILMFLVPCAAWYKGRIVPGATYSLLGLMPLLLLLALPFR 60
 DB 747 ALENLVVNLNAAASVAGTGILSLFLVPCAAWYKGRIVPGAAVYAYGVWPLLLLLALPFR 806

QY 61 AYA 63
 DB 807 AYA 809

RESULT 4
 ID Q9J3H1 PRELIMINARY; PRT; 3010 AA.
 AC Q9J3H1;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Polyprotein.
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OC NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MD21;
 RA Nagayama K., Kurosaki M., Enomoto N., Miyasaka Y., Marumo F., Sato C.;
 RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF207762; AAF65952.1; -
 DR PIR; A61196; A61196.
 DR PIR; PS0329; PS0329.
 DR HSBP; Q8UTS1; ICMX.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0008026; F:RNA-dependent helicase activity; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
 DR GO; GO:0008236; F:serine-type peptidase activity; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.

DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
 DR GO; GO:0006350; F:transcription; IEA.
 DR GO; GO:0019079; F:viral genome replication; IEA.
 DR GO; GO:0019087; F:viral transformation; IEA.
 DR InterPro; IPR000345; CytC_heme_BS.
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR011545; DEAD/DEAH_N.
 DR InterPro; IPR002522; HCV_capsid.
 DR InterPro; IPR002521; HCV_core.
 DR InterPro; IPR002519; HCV_env.
 DR InterPro; IPR002531; HCV_NS1.
 DR InterPro; IPR00745; HCV_NS4a.
 DR InterPro; IPR001490; HCV_NS4b.
 DR InterPro; IPR002868; HCV_NS5a.
 DR InterPro; IPR002166; HCV_RdRp.
 DR InterPro; IPR001650; Helicase_C.
 DR InterPro; IPR004109; Peptidase_S29.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR002518; Pept_U39_HCV_NS2.
 DR InterPro; IPR007095; RNA_pol_DS_PS.
 DR InterPro; IPR007094; RNA_pol_PSVir.
 DR Pfam; PF01543; HCV_capsid; 1.
 DR Pfam; PF01542; HCV_core; 1.
 DR Pfam; PF01539; HCV_env; 1.
 DR Pfam; PF01560; HCV_NS1; 1.
 DR Pfam; PF01538; HCV_NS2; 1.
 DR Pfam; PF02907; HCV_NS3; 1.
 DR Pfam; PF01006; HCV_NS4a; 1.
 DR Pfam; PF01001; HCV_NS4b; 1.
 DR Pfam; PF01506; HCV_NS5a; 1.
 DR Pfam; PF00271; Helicase_C; 1.
 DR Pfam; PF00998; Viral_RdRp; 1.
 DR SMART; SM00487; DEXDC; 1.
 DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
 DR Cost protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; Transmembrane.
 KM SEQUENCE 3010 AA; 327119 MW; E48938CA801B97AC CRC64;
 SQ

Query Match 86.9%; Score 284; DB 2; Length 3010;
 Best Local Similarity 85.7%; Pred. No. 2.9e-23;
 Matches 54; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 QY 1 ALENLVVNLNAAASAGTGILMFLVPCAAWYKGRIVPGATYSLLGLMPLLLLLALPFR 60
 DB 747 ALENLVVNLNAAASVAGTGILSLFLVPCAAWYKGRIVPGAAVYAYGVWPLLLLLALPFR 806

QY 61 AYA 63
 DB 807 AYA 809

RESULT 5
 ID POLG_HCVBK STANDARD; PRT; 3010 AA.
 AC P26663;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Genome polyprotein (Contains: Capsid protein C (Core protein) (P22);
 DE Envelope glycoprotein E1 (GP32) (GP35); Envelope glycoprotein E2
 DE (GP68) (GP70) (NS1); Protein P7; Nonstructural protein NS2 (P21)
 DE (EC 3.4.22.-); Protease/helicase NS3 (P70) (Hepacivirus)
 DE (EC 3.4.21.98); Nonstructural protein NS4A (P4); Nonstructural protein
 DE NS4B (P27); Nonstructural protein NS5A (P56); Nonstructural protein
 DE NS5B (P66) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].
 OS Hepatitis C virus (isolate BK) (HCV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OC NCBI_TaxID=11105;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=91140698; PubMed=1847440;
 RA Takamizawa A., Mori C., Fuke I., Manabe S., Murakami S., Fujita J.,


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FT STRAND 1120 1120
FT STRAND 1122 1122
FT STRAND 1123 1123
FT TURN 1135 1136
FT STRAND 1139 1144
FT STRAND 1149 1157
FT HELIX 1158 1161
FT TURN 1162 1163
FT TURN 1165 1166
FT STRAND 1168 1171
FT TURN 1172 1174
FT STRAND 1175 1186
FT TURN 1187 1188
FT STRAND 1189 1197
FT HELIX 1198 1202
FT TURN 1203 1204
FT STRAND 1203 1204
FT STRAND 1241 1241
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FT STRAND 1247 1247
FT HELIX 1248 1249
FT TURN 1249 1249
FT STRAND 1249 1249
FT HELIX 1249 1249
FT TURN 1250 1250
FT TURN 1251 1251
FT TURN 1253 1254
FT TURN 1259 1259
FT HELIX 1254 1258

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Query Match 86.5%; Score 283; DB 1; Length 3010;
 Best Local Similarity 85.7%; Pred. No. 3.7e-23;
 Matches 54; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

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Qy 1 ALENLVNLAASAGTHGILWLFVFCAMWYKGLVGCATYSLGLMLPLLLALPQR 60
Db 747 ALENLVNLAASAGTHGILWLFVFCAMWYKGLVGCATYSLGLMLPLLLALPQR 806
Qy 61 AYA 63
Db 807 AYA 809

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RESULT 6

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ID Q8V638 PRELIMINARY; PRT; 3010 AA.
AC Q8V638;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Polypeptide (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Fanning L.J., Itakura J., Nagayama K., Enomoto N.;
  Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF133916; AAL55821.1; -
DR PIR; A61196; A61196.
DR PIR; P00246; P00246.
DR PIR; P00804; P00804.
DR PIR; PS0329; PS0329.
DR HSP; Q8JYS1; ICWX.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.

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DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0008236; F:serine-type peptidase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR GO; GO:0019087; P:viral transformation; IEA.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
DR Pfam; PF01539; HCV_env; 1.
DR Pfam; PF01560; HCV_NS1; 1.
DR Pfam; PF01538; HCV_NS2; 1.
DR Pfam; PF02907; HCV_NS3; 1.
DR Pfam; PF01006; HCV_NS4a; 1.
DR Pfam; PF01001; HCV_NS4b; 1.
DR Pfam; PF01506; HCV_NS5a; 1.
DR Pfam; PF00271; Helicase C; 1.
DR Pfam; PF00998; Viral RdRP; 1.
DR SMART; SMO0487; DEXDC; 1.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
  Polypeptide; Transmembrane.
FT NON_TER 3010 3010
SQ SEQUENCE 3010 AA; 327182 MW; 33AAB6C07251C939 CRC64;

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Query Match 86.2%; Score 282; DB 2; Length 3010;
 Best Local Similarity 85.7%; Pred. No. 4.8e-23;
 Matches 54; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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Qy 1 ALENLVNLAASAGTHGILWLFVFCAMWYKGLVGCATYSLGLMLPLLLALPQR 60
Db 747 ALENLVNLAASAGTHGILWLFVFCAMWYKGLVGCATYSLGLMLPLLLALPQR 806
Qy 61 AYA 63
Db 807 AYA 809

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RESULT 7

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ID Q9J3F9 PRELIMINARY; PRT; 3010 AA.
AC Q9J3F9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Polypeptide.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Nagayama K., Kurosaki M., Enomoto N., Miyaoka Y., Marumo F., Sato C.;
  Submitted (NOV-1995) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF207774; AAF65964.1; -
DR PIR; A61196; A61196.
DR PIR; P00246; P00246.
DR PIR; PS0329; PS0329.
DR HSP; P26664; IHRI.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0008236; F:serine-type peptidase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

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DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR GO; GO:0019087; P:viral genome transformation; IEA.
DR InterPro; IPR000345; Cyclic_heme_BS.
DR InterPro; IPR001410; DEAD_
DR InterPro; IPR01545; DEAD/DEAH_N.
DR InterPro; IPR002522; HCV_capsid.
DR InterPro; IPR002521; HCV_core.
DR InterPro; IPR002519; HCV_env.
DR InterPro; IPR002531; HCV_NS1.
DR InterPro; IPR00745; HCV_NS4a.
DR InterPro; IPR001490; HCV_NS4b.
DR InterPro; IPR002868; HCV_NS5a.
DR InterPro; IPR002166; HCV_NS5a.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR004109; Peptidase_S29.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR002518; Pept_U39_HCV_NS2.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
DR Pfam; PF01539; HCV_env; 1.
DR Pfam; PF01560; HCV_NS1; 1.
DR Pfam; PF01538; HCV_NS2; 1.
DR Pfam; PF02907; HCV_NS3; 1.
DR Pfam; PF01006; HCV_NS4a; 1.
DR Pfam; PF01001; HCV_NS4b; 1.
DR Pfam; PF01506; HCV_NS5a; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR Pfam; PF00998; Viral_RdRp; 1.
DR SMART; SM00487; DEXDC; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
POLYPROTEIN; Transmembrane.
SQ SEQUENCE 3010 AA; 327103 MW; 7162C9DB93EE0C7 CRC64;

Query Match 86.2%; Score 282; DB 2; Length 3010;
Best Local Similarity 85.7%; Pred. No. 4.8e-23;
Matches 54; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 1 ALENVIVNAAAGTHGILWPFCAAWYKGRVPGATYSLGLWPLLLLTALPQR 60
DB 747 ALENVIVNAAASVAGSHGILWPFCAAWYKGRVPGAAVALYGVWPLLLLTALPQR 806
QY 61 AYA 63
KW |||
DB 807 AYA 809

RESULT 8
Q90IX3 PRELIMINARY; PRT; 3010 AA.
ID Q90IX3
AC Q90IX3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Polyprotein.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MD9-2;
RX MEDLINE=20013325; PubMed=10544098; DOI=10.1006/viro.1999.9924;
RA Nagayama K., Kurosaki M., Enomoto N., Maekawa S.Y., Miyasaka Y.,
Tazawa J.I., Izumi N., Maruno F., Sato C.;
RT "Time-related changes in full-length hepatitis C virus and hepatitis
activity.";
RL Virology 263:244-253(1999).
DR EMBL; AF165062; AAD56197.1; -.
DR PIR; A61196; A61196.

DR PIR; PS0329; PS0329.
DR HSSP; Q8YSL; ICWX.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0008236; F:serine-type peptidase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0006508; P:structural and peptidolysis; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR GO; GO:0019087; P:viral genome transformation; IEA.
DR InterPro; IPR000345; Cyclic_heme_BS.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR002522; HCV_capsid.
DR InterPro; IPR002521; HCV_core.
DR InterPro; IPR002519; HCV_env.
DR InterPro; IPR002531; HCV_NS1.
DR InterPro; IPR00745; HCV_NS4a.
DR InterPro; IPR001490; HCV_NS4b.
DR InterPro; IPR002868; HCV_NS5a.
DR InterPro; IPR002166; HCV_NS5a.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR004109; Peptidase_S29.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR002518; Pept_U39_HCV_NS2.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
DR Pfam; PF01539; HCV_env; 1.
DR Pfam; PF01560; HCV_NS1; 1.
DR Pfam; PF01538; HCV_NS2; 1.
DR Pfam; PF02907; HCV_NS3; 1.
DR Pfam; PF01006; HCV_NS4a; 1.
DR Pfam; PF01001; HCV_NS4b; 1.
DR Pfam; PF01506; HCV_NS5a; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR Pfam; PF00998; Viral_RdRp; 1.
DR SMART; SM00487; DEXDC; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
POLYPROTEIN; Transmembrane.
SQ SEQUENCE 3010 AA; 327254 MW; 9F1B0B3F536774FA CRC64;

Query Match 86.2%; Score 282; DB 2; Length 3010;
Best Local Similarity 85.7%; Pred. No. 4.8e-23;
Matches 54; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 1 ALENVIVNAAAGTHGILWPFCAAWYKGRVPGATYSLGLWPLLLLTALPQR 60
DB 747 ALENVIVNAAASVAGSHGILWPFCAAWYKGRVPGAAVALYGVWPLLLLTALPQR 806
QY 61 AYA 63
KW |||
DB 807 AYA 809
RESULT 9
Q98UN3 PRELIMINARY; PRT; 562 AA.
ID Q98UN3
AC Q98UN3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Polyprotein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.

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OK NCBI_TaxId=11103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20499063; PubMed=11044085;
RA DOI=10.1128/JVI.74.22.10407-10416.2000;
RA Hadlock K.G., Lefroid R.E., Perkins S., Rowe J., Yang Q., Levy S.,
RA Pilleri P., Abrightman S., Fong S.K.;
RT "Human monoclonal antibodies that inhibit binding of hepatitis C virus
RT E2 protein to CD81 and recognize conserved conformational epitopes.";
RL J. Virol. 74:10407-10416(2000).
[2]
RN SEQUENCE FROM N.A.
RA Chen M.K.C., Hadlock K.G., Yang Q., Chan L.;
RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
RL EMBL: AF348705; AAK32686.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002519; HCV env.
DR InterPro; IPR002518; Pept_U39_HCV_NS2.
DR Pfam; PF01539; HCV_env; 1.
DR Pfam; PF01560; HCV_NS1; 1.
DR Pfam; PF01538; HCV_NS2; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1 1
FT CHAIN <1 39 E1.
FT CHAIN 40 402 E2.
FT CHAIN 403 >562 p7.
FT NON_TER 562 562
SQ SEQUENCE 562 AA; 61652 MW; 9C469E9F9CCFA9DA CRC64;

Query Match 85.9%; Score 281; DB 2; Length 562;
Best Local Similarity 85.7%; Pred. No. 1.4e-23;
Matches 54; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 ALENLVNMAASAGTHGILFLVFCAMVYKGRVPGATYSLLGIMPLLLLLALPQR 60
DB 403 ALENLVNMAASVAGAHGILSLVFCAMVYIKGRVPGAAVALYGVWPLLLLLALPQR 462
QY 61 AYA 63
DB 463 AYA 465

RESULT 10
O80P91 PRELIMINARY; PRT; 1117 AA.
ID O80P91;
AC O80P91;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polyprotein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepcivirinae.
OC NCBI_TaxId=11103;
OX NCBI_TaxId=11103;
RP SEQUENCE FROM N.A.
RX MEDLINE=21904745; PubMed=11907242;
RA DOI=10.1128/JVI.76.8.4034-4043.2002;
RA Kalinina O., Norder H., Mukomolov S., Magnus L.O.;
RT "A natural intergenotypic recombinant of hepatitis C virus identified
RT in St. Petersburg.";
RL J. Virol. 76:4034-4043(2002).
DR EMBL; AY070174; AAL50213.1; -.
DR HSBP; G91R04; 1B77.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.

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DR GO; GO:0008236; F:serine-type peptidase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0019087; P:viral transformation; IEA.
DR InterPro; IPR002522; HCV_capsid.
DR InterPro; IPR002519; HCV_core.
DR InterPro; IPR002519; HCV_NS1.
DR InterPro; IPR004109; Peptidase_S29.
DR InterPro; IPR002518; Pept_U39_HCV_NS2.
DR Pfam; PF01543; HCV_capsid; 1.
DR Pfam; PF01542; HCV_core; 1.
DR Pfam; PF01539; HCV_core; 1.
DR Pfam; PF01560; HCV_NS1; 1.
DR Pfam; PF01538; HCV_NS2; 1.
DR Pfam; PF02907; HCV_NS3; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1117 1117
SQ SEQUENCE 1117 AA; 121723 MW; 892B814C073656A8 CRC64;

Query Match 85.9%; Score 281; DB 2; Length 1117;
Best Local Similarity 85.7%; Pred. No. 2.6e-23;
Matches 54; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 ALENLVNMAASAGTHGILFLVFCAMVYKGRVPGATYSLLGIMPLLLLLALPQR 60
DB 747 ALENLVNMAASVAGAHGILSLVFCAMVYIKGRVPGAAVALYGVWPLLLLLALPQR 806
QY 61 AYA 63
DB 807 AYA 809

RESULT 11
O68826 PRELIMINARY; PRT; 3010 AA.
ID O68826;
AC O68826;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polyprotein.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepcivirinae.
OC NCBI_TaxId=11103;
OX NCBI_TaxId=11103;
RP SEQUENCE FROM N.A.
RX CHO M.J.;
RL Submitted (SEP-1991) to the EMBL/Genbank/DBJ databases.
RL EMBL; D14484; BAA03375.1; -.
DR PIR; A61196; A61196.
DR PIR; P00246; P00246.
DR PIR; P00804; P00804.
DR PIR; P00329; P00329.
DR HSBP; O8JYS1; 1CWK.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0003722; F:RNA binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0008236; F:serine-type peptidase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR GO; GO:0019087; P:viral transformation; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH_N.

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DR InterPro: IPR002522; HCV_capsid.
DR InterPro: IPR002521; HCV_core.
DR InterPro: IPR002519; HCV_env.
DR InterPro: IPR002531; HCV_NS1.
DR InterPro: IPR007045; HCV_NS4a.
DR InterPro: IPR001490; HCV_NS5a.
DR InterPro: IPR002868; HCV_NS5b.
DR InterPro: IPR002166; HCV_RdRp.
DR InterPro: IPR001650; Helicase_C.
DR InterPro: IPR004109; Peptidase_S29.
DR InterPro: IPR009003; Pept_Ser_Cys.
DR InterPro: IPR002518; Pept_U39_HCV_NS2.
DR InterPro: IPR007095; RNA_pol_DS_PS.
DR InterPro: IPR007094; RNA_pol_PSVir.
DR Pfam: PF01543; HCV_capsid; 1.
DR Pfam: PF01542; HCV_core; 1.
DR Pfam: PF01539; HCV_env; 1.
DR Pfam: PF01560; HCV_NS1; 1.
DR Pfam: PF01538; HCV_NS2; 1.
DR Pfam: PF02907; HCV_NS3; 1.
DR Pfam: PF01006; HCV_NS4a; 1.
DR Pfam: PF01001; HCV_NS4b; 1.
DR Pfam: PF01506; HCV_NS5a; 1.
DR Pfam: PF00271; Helicase_C; 1.
DR Pfam: PF00998; Viral_RdRp; 1.
DR SMART: SM00487; DEXDC; 1.
DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
SQ SEQUENCE 3010 AA; 327151 MW; 7270F47984554FAD CRC64;

Query Match 85.9%; Score 281; DB 2; Length 3010;
Best Local Similarity 85.7%; Pred. No. 6.3e-23;
Matches 54; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 ALENLVNNAASAGTHGILWLFVFCAMVYKGRVPGATYSLGLWPLLLLLLALPQR 60
DB 747 ALENLVNNAASVAGAHGILSLVFPCCAWYIKGRVPGAAVALGVWPLLLLLLALPQR 806

QY 61 AYA 63
DB 807 AYA 809

RESULT 12
OG6YR9 PRELIMINARY; PRT; 3010 AA.
ID OG6YR9;
AC OG6YR9;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Polyprotein.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus;
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NS89;
RX PubMed=15218169; DOI=10.1099/vir.0.79984-0;
RA Kalinina O., Norder H., Magnius L.O.;
RT "Full-length open reading frame of a recombinant hepatitis C virus
strain from St Petersburg: proposed mechanism for its formation.";
RL J. Gen. Virol. 85:1853-1857(2004).
DR EMBL: AY587844; C: integral to membrane; IEA.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0019028; C: viral capsid; IEA.
DR GO: GO:0019031; C: viral envelope; IEA.
DR GO: GO:0005524; F: ATP binding; IEA.
DR GO: GO:0008026; F: ATP-dependent helicase activity; IEA.
DR GO: GO:0016787; F: hydrolase activity; IEA.
DR GO: GO:0003723; F: RNA binding; IEA.
DR GO: GO:0003968; F: RNA-directed RNA polymerase activity; IEA.
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DR GO: GO:0008236; F: serine-type peptidase activity; IEA.
DR GO: GO:0005198; F: structural molecule activity; IEA.
DR GO: GO:0006508; F: proteolysis and peptidolysis; IEA.
DR GO: GO:0006350; P: transcription; IEA.
DR GO: GO:0019079; P: viral genome replication; IEA.
DR GO: GO:0019087; P: viral transformation; IEA.
DR InterPro: IPR000345; CytC_heme_BS.
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR011545; DEAD/DEAH_N.
DR InterPro: IPR002522; HCV_capsid.
DR InterPro: IPR002521; HCV_core.
DR InterPro: IPR002519; HCV_env.
DR InterPro: IPR002531; HCV_NS1.
DR InterPro: IPR007045; HCV_NS4a.
DR InterPro: IPR001490; HCV_NS4b.
DR InterPro: IPR002868; HCV_NS5a.
DR InterPro: IPR002166; HCV_RdRp.
DR InterPro: IPR001650; Helicase_C.
DR InterPro: IPR004109; Peptidase_S29.
DR InterPro: IPR009003; Pept_Ser_Cys.
DR InterPro: IPR002518; Pept_U39_HCV_NS2.
DR InterPro: IPR007095; RNA_pol_DS_PS.
DR InterPro: IPR007094; RNA_pol_PSVir.
DR Pfam: PF01543; HCV_capsid; 1.
DR Pfam: PF01542; HCV_core; 1.
DR Pfam: PF01539; HCV_env; 1.
DR Pfam: PF01560; HCV_NS1; 1.
DR Pfam: PF01538; HCV_NS2; 1.
DR Pfam: PF02907; HCV_NS3; 1.
DR Pfam: PF01006; HCV_NS4a; 1.
DR Pfam: PF01001; HCV_NS4b; 1.
DR Pfam: PF01506; HCV_NS5a; 1.
DR Pfam: PF00271; Helicase_C; 1.
DR Pfam: PF00998; Viral_RdRp; 1.
DR SMART: SM00487; DEXDC; 1.
DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
KW ATP-binding; Coat protein; Envelope protein; Glycoprotein; Helicase;
KW Hydrophobic; Nonstructural protein; Polyprotein; Transmembrane.
SQ SEQUENCE 3010 AA; 326545 MW; D05AB2897F142A58 CRC64;

Query Match 85.9%; Score 281; DB 2; Length 3010;
Best Local Similarity 85.7%; Pred. No. 6.3e-23;
Matches 54; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 ALENLVNNAASAGTHGILWLFVFCAMVYKGRVPGATYSLGLWPLLLLLLALPQR 60
DB 747 ALENLVNNAASVAGAHGILSLVFPCCAWYIKGRVPGAAVALGVWPLLLLLLALPQR 806

QY 61 AYA 63
DB 807 AYA 809

RESULT 13
Q9DTE1 PRELIMINARY; PRT; 3010 AA.
ID Q9DTE1;
AC Q9DTE1;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Polyprotein.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus;
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUES=Serum;
RA Takahashi K., Iwata K., Matsumoto M., Matsumoto H., Nakao K.,
Hachihara T., Ohta Y., Kanai K., Maruo H., Baba K., Hijikata M.,
Mishiro S.;
RT "Hepatitis C virus (HCV) genotype 1b sequences from fifteen patients
```

RT with hepatocellular carcinoma: the 'progression score' revisited."
RL Hepatol. Res. 20:161-171 (2001).
DR EMBL/ AB049096; BAB18809.1; -
DR PIR/ A61196; A61196.
DR PIR/ P00246; P00246.
DR PIR/ P00252; P00252.
DR PIR/ P00253; P00253.
DR PIR/ P00254; P00254.
DR PIR/ P00804; P00804.
DR HSSP/ Q8JYS1; 1CMX.
DR GO/ GO:0016021; C:Integral to membrane; IEA.
DR GO/ GO:0019028; C:viral capsid; IEA.
DR GO/ GO:0019031; C:viral envelope; IEA.
DR GO/ GO:0005524; F:ATP binding; IEA.
DR GO/ GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO/ GO:0003723; F:RNA binding; IEA.
DR GO/ GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO/ GO:0008236; F:serine-type peptidase activity; IEA.
DR GO/ GO:0005198; F:structural molecule activity; IEA.
DR GO/ GO:0006508; F:proteolysis and peptidolysis; IEA.
DR GO/ GO:0006350; P:transcription; IEA.
DR GO/ GO:0019079; P:viral genome replication; IEA.
DR GO/ GO:0019087; P:viral transformation; IEA.
DR InterPro/ IPR000345; Cytochrome_B5.
DR InterPro/ IPR001410; DEAD.
DR InterPro/ IPR002521; HCV_core.
DR InterPro/ IPR002521; HCV_core.
DR InterPro/ IPR002519; HCV_env.
DR InterPro/ IPR002531; HCV_NS1.
DR InterPro/ IPR000745; HCV_NS4a.
DR InterPro/ IPR001490; HCV_NS4b.
DR InterPro/ IPR002868; HCV_NS5a.
DR InterPro/ IPR002166; HCV_RdRP.
DR InterPro/ IPR001650; Helicase_C.
DR InterPro/ IPR004109; Peptidase_S29.
DR InterPro/ IPR009003; Peptidase_S29.
DR InterPro/ IPR002518; Peptidase_S29.
DR InterPro/ IPR007095; RNA_pol_DS_PS.
DR InterPro/ IPR007094; RNA_pol_PSVir.
DR Pfam/ PF01543; HCV_capsid; 1.
DR Pfam/ PF01543; HCV_core; 1.
DR Pfam/ PF01539; HCV_env; 1.
DR Pfam/ PF01560; HCV_NS1; 1.
DR Pfam/ PF01538; HCV_NS2; 1.
DR Pfam/ PF02907; HCV_NS3; 1.
DR Pfam/ PF01006; HCV_NS4a; 1.
DR Pfam/ PF01001; HCV_NS4b; 1.
DR Pfam/ PF01506; HCV_NS5a; 1.
DR Pfam/ PF00271; Helicase_C; 1.
DR Pfam/ PF00998; Viral_RdRP; 1.
DR SMART/ SM00487; DEXDC; 1.
DR PROSITE/ PS00190; CYTOCHROME_C; UNKNOWN_1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
SQ SEQUENCE 3010 AA; 326845 MW; 90457AC819A32150 CRC64;
Query Match 85.9%; Score 281; DB 2; Length 3010;
Best Local Similarity 85.7%; Pred. No. 6.3e-23;
Matches 54; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 1 ALENLVVNLNAAAGTGILMFLVFCAMVYKGRVPGATYSILGLMPILLILLALPQR 60
DB 747 ALENLVVNLNAAAGTGILMFLVFCAMVYKGRVPGATYSILGLMPILLILLALPQR 806
QY 61 AYA 63
DB 807 AYA 809

AC Q9J3G3;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DR 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-MAR-2004 (Tremblrel. 26, Last annotation update)
OS Polyprotein.
OC Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCB1_Taxid=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MD29;
RA Nagayama K., Kurosaki M., Enomoto N., Miyasaka Y., Maruno F., Sato C.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL/ AF207770; AAF65960.1; -
DR PIR/ A61196; A61196.
DR PIR/ P00246; P00246.
DR PIR/ P00252; P00252.
DR HSSP/ Q8JYS1; 1CMX.
DR GO/ GO:0016021; C:Integral to membrane; IEA.
DR GO/ GO:0019028; C:viral capsid; IEA.
DR GO/ GO:0019031; C:viral envelope; IEA.
DR GO/ GO:0005524; F:ATP binding; IEA.
DR GO/ GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO/ GO:0003723; F:RNA binding; IEA.
DR GO/ GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO/ GO:0008236; F:serine-type peptidase activity; IEA.
DR GO/ GO:0005198; F:structural molecule activity; IEA.
DR GO/ GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO/ GO:0006350; P:transcription; IEA.
DR GO/ GO:0019079; P:viral genome replication; IEA.
DR GO/ GO:0019087; P:viral transformation; IEA.
DR InterPro/ IPR000345; Cytochrome_B5.
DR InterPro/ IPR001410; DEAD.
DR InterPro/ IPR001545; DEAD/DEAH_N.
DR InterPro/ IPR002521; HCV_core.
DR InterPro/ IPR002521; HCV_core.
DR InterPro/ IPR002519; HCV_env.
DR InterPro/ IPR002531; HCV_NS1.
DR InterPro/ IPR000745; HCV_NS4a.
DR InterPro/ IPR002868; HCV_NS5a.
DR InterPro/ IPR001490; HCV_NS4b.
DR InterPro/ IPR002166; HCV_RdRP.
DR InterPro/ IPR004109; Peptidase_S29.
DR InterPro/ IPR009003; Peptidase_S29.
DR InterPro/ IPR002518; Peptidase_S29.
DR InterPro/ IPR007095; RNA_pol_DS_PS.
DR InterPro/ IPR007094; RNA_pol_PSVir.
DR Pfam/ PF01543; HCV_capsid; 1.
DR Pfam/ PF01539; HCV_core; 1.
DR Pfam/ PF01560; HCV_NS1; 1.
DR Pfam/ PF01538; HCV_NS2; 1.
DR Pfam/ PF02907; HCV_NS3; 1.
DR Pfam/ PF01006; HCV_NS4a; 1.
DR Pfam/ PF01001; HCV_NS4b; 1.
DR Pfam/ PF01506; HCV_NS5a; 1.
DR Pfam/ PF00998; Viral_RdRP; 1.
DR SMART/ SM00487; DEXDC; 1.
DR PROSITE/ PS00190; CYTOCHROME_C; UNKNOWN_1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
SQ SEQUENCE 3010 AA; 327227 MW; 19783535650CACE3 CRC64;
Query Match 85.9%; Score 281; DB 2; Length 3010;
Best Local Similarity 85.7%; Pred. No. 6.3e-23;
Matches 54; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 1 ALENLVVNLNAAAGTGILMFLVFCAMVYKGRVPGATYSILGLMPILLILLALPQR 60
DB 747 ALENLVVNLNAAAGTGILMFLVFCAMVYKGRVPGATYSILGLMPILLILLALPQR 806
QY 61 AYA 63

DB 807 AYA 809

RESULT 15

09J3G6 PRELIMINARY; PRT; 3010 AA.

AC 09J3G6, 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Polypeptide.

OS Hepatitis C virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

OC Hepacivirus.

OX NCBI_TaxID=11103;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MD26;

RA Nagayama K., Kurosaki M., Enomoto N., Miyasaka Y., Marumo F., Sato C.,

RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF207767; AAF65957.1; -.

DR PIR; A61196; A61196.

DR PIR; P00246; P00246.

DR PIR; P00254; P00254.

DR PIR; P50329; P50329.

DR HSSP; Q8JYS1; ICWX.

DR MEROPS; S29.002; -.

DR GO; GO:0016021; C: integral to membrane; IEA.

DR GO; GO:0019028; C: viral capsid; IEA.

DR GO; GO:0019031; C: viral envelope; IEA.

DR GO; GO:0005524; F: ATP binding; IEA.

DR GO; GO:0008026; F: ATP-dependent helicase activity; IEA.

DR GO; GO:0003723; F: RNA binding; IEA.

DR GO; GO:0003968; F: RNA-directed RNA polymerase activity; IEA.

DR GO; GO:0008236; F: serine-type peptidase activity; IEA.

DR GO; GO:0005198; F: structural molecule activity; IEA.

DR GO; GO:0006508; P: proteolysis and peptidolysis; IEA.

DR GO; GO:0006350; P: transcription; IEA.

DR GO; GO:0019079; P: viral genome replication; IEA.

DR GO; GO:0019087; P: viral transformation; IEA.

DR InterPro; IPR000345; CytC_heme_BS.

DR InterPro; IPR001410; DEAD.

DR InterPro; IPR011345; DEAD/DEAH_N.

DR InterPro; IPR002522; HCV_capsid.

DR InterPro; IPR002521; HCV_core.

DR InterPro; IPR002519; HCV_env.

DR InterPro; IPR000745; HCV_NS1.

DR InterPro; IPR001490; HCV_NS4a.

DR InterPro; IPR001490; HCV_NS4b.

DR InterPro; IPR002868; HCV_NS5a.

DR InterPro; IPR002166; HCV_RdRp.

DR InterPro; IPR001650; Helicase_C.

DR InterPro; IPR004109; Peptidase_S29.

DR InterPro; IPR009003; Pept_Ser_Cys.

DR InterPro; IPR002518; Pept_U3_HCV_NS2.

DR InterPro; IPR007095; RNA_pol_DS_PS.

DR InterPro; IPR007094; RNA_pol_PSVir.

DR Pfam; PF01543; HCV_capsid; 1.

DR Pfam; PF01542; HCV_core; 1.

DR Pfam; PF01539; HCV_env; 1.

DR Pfam; PF01560; HCV_NS1; 1.

DR Pfam; PF01538; HCV_NS2; 1.

DR Pfam; PF02907; HCV_NS3; 1.

DR Pfam; PF01006; HCV_NS4a; 1.

DR Pfam; PF01001; HCV_NS4b; 1.

DR Pfam; PF01506; HCV_NS5a; 1.

DR Pfam; PF00271; Helicase_C1; 1.

DR Pfam; PF00998; Viral_RdRp; 1.

DR SMART; SM00487; DEXDC; 1.

DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.

DR Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;

KW Polypeptide; Transmembrane.

SQ SEQUENCE 3010 AA; 327166 MW; 74FAB6B80F24837B CRC64;

Query Match 85.9%; Score 281; DB 2; Length 3010;

Best Local Similarity 85.7%; Pred. No. 6.3e-23;

Matches 54; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 ALENLVNNAASAGTHGILWELVFPCAAMVKGRIVPGATYSILGLTPILLILLALPPR 60

DB 747 ALENLVNNAASVAGAHGILSLVFPCAAMVIRKGLVPGAAVALYGVMPILLILLALPPR 806

QY 61 AYA 63

DB 807 AYA 809

Search completed: October 4, 2005, 18:57.32

Job time : 65 secs